

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2004, 17:36:30 ; Search time 6138 Seconds
(without alignments)
11651.991 Million cell updates/sec

Title: US-10-036-150-44
Perfect score: 2395
Sequence: 1 cctggagcgggaagcgccg.....gcaataattgagaaaaaaa 2395

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : EST:*

1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estmu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_htc:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_htc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estom:*
17:	em_gss_hum:*
18:	em_gss_inv:*
19:	em_gss_pln:*
20:	em_gss_vrt:*
21:	em_gss_fun:*
22:	em_gss_mam:*
23:	em_gss_mus:*
24:	em_gss_pro:*
25:	em_gss_rod:*
26:	em_gss_phg:*
27:	em_gss_vrl:*
28:	gb_gss1:*
29:	gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	710.8	29.7	1201 13 BX377108
C 2	706.4	29.5	723 14 CA308767
C 3	704.6	29.4	731 13 BU622377
4	698.6	29.2	935 12 BI771815

5	682.6	28.5	825	14	CF594116
6	662.2	27.6	809	12	BG171457
7	655.6	27.4	905	13	BU191836
8	646.4	27.0	971	14	CF593551
C 9	557.2	23.3	585	12	BQ001548
10	554.2	23.1	615	9	AL703949
11	519.2	21.7	801	12	BG742889
12	513.8	21.5	1089	12	BM920390
13	458.4	19.1	909	14	CD517899
14	439.8	18.4	546	9	AL698226
C 15	434.6	18.1	441	9	AI521101
C 16	405	16.9	418	28	AQ673215
17	395.2	16.5	434	10	BE549374
C 18	388.8	16.2	1201	13	BX377107
C 19	371.8	15.5	390	13	BX097186
20	370.8	15.4	640	13	BU425116
21	355.2	14.8	920	12	BG336024
22	355.2	14.8	970	12	BG336399
23	335	14.0	557	10	BE757899
C 24	312.2	13.0	368	10	AW262524
25	309.2	12.9	332	12	BM844459
26	308.4	12.9	595	12	BG346870
27	304	12.7	570	10	BE669243
C 28	303.6	12.7	405	10	AW262485
C 29	300.8	12.6	739	14	CA377408
C 30	300.6	12.6	319	9	AA687924
31	291.6	12.2	412	12	BM107678
32	280.8	11.7	631	9	AL871903
33	276.8	11.6	753	12	BI919095
34	264.2	11.0	508	14	CB783017
35	263	11.0	674	12	BG927822
36	248.4	10.4	418	14	CB765650
37	239	10.0	510	14	CB548333
38	237.4	9.9	253	9	AA361388
39	216.4	9.0	253	14	T32542
C 40	206.2	8.6	350	13	BQ293001
41	206	8.6	976	14	CD516167
42	205	8.6	1205	10	BF791461
43	204	8.5	318	14	Z44206
44	199	8.3	1099	12	BM455257
45	192.4	8.0	789	12	BG389289
C 46	184	7.7	318	12	BI051441
47	177	7.4	806	12	BG923173
48	177	7.4	3150	11	BC051059
49	172.6	7.2	355	10	BF746141
C 50	165.2	6.9	264	12	BI026475
51	163.4	6.8	764	13	BX077539
52	162.4	6.8	501	29	CG592530
53	160.4	6.7	252	9	AA356939
54	152.8	6.4	739	13	BU130677
55	150.6	6.3	517	12	BI391754
C 56	135.2	5.6	744	13	BX077538
57	116.4	4.9	460	10	BF442617
58	112.6	4.7	510	9	AL913388
59	110.4	4.6	720	29	CE024824
60	107.4	4.5	122	13	BQ360060
61	107.4	4.5	934	10	BE897861
62	106.8	4.5	556	12	BM323673
63	106.8	4.5	651	13	BQ522572
64	102	4.3	466	28	BZ270849
65	101.8	4.3	990	12	BM468049
66	101.8	4.3	2495	11	BC036916
67	101.8	4.3	3270	29	AY408630
68	101.2	4.2	758	12	BI080925
C 69	99.4	4.0	560	12	BJ434815
70	96.6	4.0	880	14	CD387014
71	96.2	4.0	3270	29	AY408631
72	93.8	3.9	545	10	AW862654
73	90.6	3.8	3282	29	AY408632
74	89	3.7	124	10	BE685541
75	87.8	3.7	140	14	CD733602
76	87.4	3.6	929	13	BU151896
C 77	86.8	3.6	608	28	BZ296288

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78	85	927	13	BU107863	BU107863	602954132	151	42.4	1.8	677	10	BB654609
79	83.6	515	12	BJ002551	BJ002551	BJ002551	152	42.2	1.8	1201	13	BX396032
80	83.4	821	12	BI102658	BI102658	602888212	153	42	1.8	645	29	CNS01213
81	83.2	798	13	BU237135	BU237135	603410865	154	42	1.8	925	29	CNS0091P
82	82	837	28	BH164427	BH164427	ENTSG01TF	155	41.6	1.7	401	28	AQ845931
83	82	842	13	BU955911	BU955911	AGENCOURT	156	41.6	1.7	515	13	BX424977
84	82	914	13	BQ960346	BQ960346	AGENCOURT	157	41.4	1.7	1201	9	AL531027
85	80.4	891	13	AZ544326	AZ544326	ENTDQ74TR	158	41.4	1.7	1201	13	BX381961
86	80.2	773	14	CF271629	CF271629	AGENCOURT	159	41.2	1.7	473	28	AZ050509
87	78.2	807	12	BI768432	BI768432	603053895	160	41.2	1.7	554	28	BH197929
88	77.2	652	9	AV962249	AV962249	AV962249	161	41.2	1.7	565	28	BH195242
89	77	922	28	AZ541397	AZ541397	ENTGT63TR	162	41.2	1.7	603	12	BI631378
90	76.6	3578	11	AK050819	AK050819	Mus muscu	163	41.2	1.7	644	9	AI107888
91	74.2	652	10	BF980965	BF980965	602310127	164	41.2	1.7	671	12	BI605387
92	74.2	689	13	BW257468	BW257468	BW257468	165	41	1.7	951	9	AL555760
93	74.2	981	29	CNS06HN3	CNS06HN3	T7 end of	166	40.8	1.7	962	13	BX415131
94	73.8	765	14	CF271610	CF271610	AGENCOURT	167	40.2	1.7	460	14	CB738088
95	72.2	789	12	BI907424	BI907424	603063796	168	40.2	1.7	505	13	BU664768
96	71.6	490	29	CG498720	CG498720	OST40216	169	40.2	1.7	696	13	BY733512
97	71.6	528	10	AW907889	AW907889	ur94f08.Y	170	40.2	1.7	723	28	AQ362027
98	70.8	585	10	AW870081	AW870081	NXNV 123	171	40.2	1.7	785	28	AQ324174
99	69.8	625	12	BJ095097	BJ095097	BJ095097	172	40.2	1.7	994	13	BX414650
100	67.4	905	14	CA975938	CA975938	AGENCOURT	173	40.2	1.7	1026	28	BZ569417
101	67.4	959	12	BM048802	BM048802	603628344	174	40.2	1.7	1171	13	BX342087
102	66.8	606	9	AL680763	AL680763	AL680763	175	40.2	1.7	1201	13	BX360624
103	66.6	941	10	BF304258	BF304258	601887129	176	40	1.7	884	13	BQ947303
104	66.6	378	10	AW693601	AW693601	NF066A08S	177	40	1.7	887	9	AL524426
105	64.4	817	28	BH370057	BH370057	AG-ND-175	178	40	1.7	966	28	AZ675567
106	63.6	830	10	BE822616	BE822616	GM700018B	179	40	1.7	1200	13	BX415896
107	63.2	998	14	CB184052	CB184052	AGENCOURT	180	40	1.7	1201	13	BX381961
108	62.8	771	12	BG861700	BG861700	602795284	181	40	1.7	1579	12	BG759656
109	62.8	714	12	BG396419	BG396419	602459134	182	39.8	1.7	1000	13	BX407619
110	59.6	875	13	BU195561	BU195561	AGENCOURT	183	39.8	1.7	1093	13	BQ939664
111	59.4	580	14	CB388012	CB388012	OSTF090D1	184	39.6	1.7	1201	13	BX406090
112	59.2	684	9	AI387560	AI387560	GH18119.5	185	39.6	1.7	665	12	BI625905
113	58.6	435	10	BE909527	BE909527	601502887	186	39.6	1.7	754	13	BU105063
114	58.6	576	12	BM723055	BM723055	UI-E-E01-	187	39.6	1.7	844	29	CNS0052P
115	58.6	636	10	BE258528	BE258528	601117095	188	39.6	1.7	898	13	BX390870
116	58.6	724	12	BI818120	BI818120	603032341	189	39.4	1.6	904	29	CNS06GZY
117	57.2	285	12	BI399486	BI399486	MI-P-Ayl-	190	39.4	1.6	507	28	AQ682429
118	55.4	216	9	AL863354	AL863354	AL863354	191	39.4	1.6	599	12	BM566094
119	54.8	911	28	BH150812	BH150812	ENTPL76TR	192	39.4	1.6	831	12	BI755336
120	53.8	400	14	CD563952	CD563952	B0471F05-	193	39.4	1.6	1126	13	BX446391
121	52.8	1019	29	CNS05Q75	CNS05Q75	AL348890	194	39.2	1.6	652	14	CA297260
122	52.2	572	12	BJ111192	BJ111192	Tetraodon	195	39.2	1.6	661	14	CA285706
123	52.2	666	13	BY724544	BY724544	BY724544	196	39.2	1.6	699	14	CA285594
124	51	413	14	CD563688	CD563688	B0467E12-	197	39.2	1.6	768	14	CA272154
125	50.8	681	10	BE261576	BE261576	601149287	198	39.2	1.6	928	10	BF206830
126	50.6	510	29	CG809849	CG809849	FSAAN18TF	199	39	1.6	559	13	BX384405
127	50.2	651	29	LBFAF022H08	LBFAF022H08	BX538441	200	38.8	1.6	474	28	BZ949684
128	49.6	776	12	BI760755	BI760755	Leishmani	201	38.8	1.6	552	13	BU497908
129	46.8	655	10	BE262625	BE262625	601149785	202	38.8	1.6	712	13	BX416727
130	46.8	961	29	CNS074QX	CNS074QX	UI-M-FW0-	203	38.8	1.6	1090	12	BI556767
131	46	807	14	CA316535	CA316535	CSU-K33r.	204	38.8	1.6	1106	29	AG163789
132	45.6	993	28	CC071242	CC071242	BW241247	205	38.8	1.6	1201	13	BX356664
133	45.2	542	13	BW241247	BW241247	BE3112721	206	38.6	1.6	325	29	CE817664
134	45.2	772	10	BE3112721	BE3112721	601149685	207	38.6	1.6	385	10	AW354542
135	44.4	383	13	BQ559480	BQ559480	H4058D08-	208	38.6	1.6	706	29	CE696456
136	44.4	426	14	CA542701	CA542701	C0622G08-	209	38.6	1.6	733	28	BZ092510
137	44.4	689	10	BE273942	BE273942	601104589	210	38.6	1.6	846	29	CNS010RJ
138	44.2	620	13	BU434402	BU434402	603257452	211	38.6	1.6	866	29	CG966996
139	44.2	779	13	BU477257	BU477257	603841840	212	38.6	1.6	1077	29	CNS046AA
140	44.2	1201	9	AL538546	AL538546	AL538546	213	38.6	1.6	1155	13	BX444199
141	43.8	616	9	AI389051	AI389051	GH20132.5	214	38.6	1.6	1159	29	CNS015XR
142	43.6	360	9	AA715117	AA715117	nv10a02.8	215	38.4	1.6	468	29	CE527691
143	43	651	12	BM487513	BM487513	pgm2n.pk0	216	38.4	1.6	672	28	BH888571
144	43	675	14	CA199275	CA199275	SCRLF101	217	38.4	1.6	720	29	CE228270
145	43	748	14	CA223138	CA223138	SCJFFL1C0	218	38.4	1.6	765	28	BZ1303
146	43	779	13	BQ571536	BQ571536	UI-M-FC0-	219	38.4	1.6	894	28	AZ543408
147	43	781	14	CF742708	CF742708	UI-M-HB0-	220	38.4	1.6	902	29	CNS006QP
148	43	839	29	CNS004NB	CNS004NB	Drosophil	221	38.4	1.6	1201	29	CNS016BR
149	43	930	13	BQ926589	BQ926589	AGENCOURT	222	38.4	1.6	1451	10	BF688440
150	42.6	852	13	BX393687	BX393687	BX393687	223	38.2	1.6	484	28	BZ906389

BB654609 BB654609
BX396032 BX396032
AL101589 Drosophil
AL053013 Drosophil
AQ845931 LMAJFV1_1
BX424977 BX424977
AL531027 AL531027
BX381961 BX381961
AZ050509 GSSTC1135
BH197929 TC3-59D9
BH195242 TC3-33G10
BI631378 RH60932.5
AI107888 GH05767.5
BI605387 RH70978.5
AL555760 AL555760
BX415131 BX415131
CB738088 AMGNNUC:M
BU664768 cl122C08.
BY733512 BY733512
AQ362027 mgxb0004I
AQ324174 mgxb00170
BX414650 BX414650
BZ569417 pac2-164
EX342087 BX342087
BX360624 BX360624
BQ947303 AGENCOURT
AL524426 AL524426
AZ675567 ENTFN17TF
BX415896 BX415896
BX381961 BX381961
BG759656 602713349
BX407619 BX407619
BQ939664 AGENCOURT
BX406090 BX406090
BI625905 RH66413.5
BU105063 603004980
AL056652 Drosophil
BX390870 BX390870
AL398372 T7 end of
AQ682429 HS_5520_A
BM566094 rs95a03.Y
BI755336 603024953
BX446391 BX446391
CA297260 SCUTSD208
CA285706 SCEZSD107
CA285594 SCEZSD107
CA272154 SCVPLB208
BF206830 601870234
BX384405 BX384405
BZ949684 CH240_38G
BU497908 PfESToab8
BX416727 BX416727
BI556767 603239489
AG163789 Pan trogl
BX356664 BX356664
CE817664 tigr-gss-
AW354542 36514 MAR
CE696456 tigr-gss-
BZ092510 CH230-140
AL099337 Drosophil
CG966996 MBEEP49TF
AL276427 Tetraodon
BX444199 BX444199
AL106041 Drosophil
CE527691 tigr-gss-
BH888571 Gm_UMD001
CE228270 tigr-gss-
BZ1303 T27C6-T7 TA
AZ543408 ENTGI32TR
AL065804 Drosophil
AL106545 Drosophil
BF688440 602185038
BZ906389 CH240_29C

C 224	38.2	1.6	643	28	AZ312003	AZ312003 1M0027I07	297	37.4	1.6	1425	11	BC018607	BC018607 Homo sapi
C 225	38.2	1.6	673	10	BE260998	BE260998 601149935	298	37.4	1.6	2072	29	AY411198	AY411198 Homo sapi
226	38.2	1.6	736	28	BZ020145	BZ020145 oee40a05.	299	37.2	1.6	431	13	BQ809016	BQ809016 1030008E1
227	38.2	1.6	744	14	CF869175	CF869175 tric018xd	300	37.2	1.6	435	29	CE626826	CE626826 tigr-gss-
228	38.2	1.6	824	14	CB899301	CB899301 tric018xd	301	37.2	1.6	454	10	BE761471	BE761471 894099D08
229	38.2	1.6	839	29	CNS004NB	AL054280 Drosophil	302	37.2	1.6	456	9	AA962623	AA962623 om82b05.s
230	38.2	1.6	910	29	CNS006ON	AL065629 Drosophil	303	37.2	1.6	541	14	CA200155	CA200155 SCRUF1102
231	38.2	1.6	1201	29	CNS0141B	AL103577 Drosophil	304	37.2	1.6	568	29	CE193316	CE193316 tigr-gss-
C 232	38	1.6	251	10	BF874248	BF874248 IL3-ET011	305	37.2	1.6	629	12	BI873549	BI873549 963109F05
C 233	38	1.6	317	13	BX621843	BX621843 BX621843	306	37.2	1.6	642	29	CE647396	CE647396 tigr-gss-
C 234	38	1.6	538	29	CE409983	CE409983 tigr-gss-	307	37.2	1.6	672	10	AW950474	AW950474 EST362544
C 235	38	1.6	1201	9	AL564081	AL564081 AL564081	308	37.2	1.6	672	13	BU651153	BU651153 1112091F0
C 236	38	1.6	1273	12	BG256643	BG256643 602370825	309	37.2	1.6	690	13	BQ815678	BQ815678 1030052B0
C 237	37.8	1.6	584	12	BM320685	BM320685 rs92908.Y	310	37.2	1.6	721	12	BG860698	BG860698 1024072C1
C 238	37.8	1.6	879	12	BG621829	BG621829 602619694	311	37.2	1.6	746	12	BG845290	BG845290 1024009F0
C 239	37.8	1.6	922	13	BX462312	BX462312 BX462312	C 312	37.2	1.6	1201	9	AL524337	AL524337 AL524337
C 240	37.8	1.6	996	9	AL546967	AL546967 AL546967	313	37.2	1.6	1201	9	AL524338	AL524338 AL524338
C 241	37.8	1.6	1024	12	BG388919	BG388919 602414664	C 314	37.2	1.6	1201	9	AL563716	AL563716 AL563716
C 242	37.8	1.6	1201	9	AL553735	AL553735 AL553735	315	37.2	1.6	1201	13	BX387714	BX387714 BX387714
C 243	37.6	1.6	508	12	BI531929	BI531929 1024117F0	C 316	37	1.5	278	9	AL372209	AL372209 MtBA49D01
C 244	37.6	1.6	646	28	AZ636767	AZ636767 1M0495JL3	317	37	1.5	412	13	BY285359	BY285359 BY285359
C 245	37.6	1.6	692	12	BP136028	BP136028 BP136028	318	37	1.5	422	12	BM753262	BM753262 K-EST0030
C 246	37.6	1.6	840	28	BH770401	BH770401 LLMtag17	C 319	37	1.5	457	14	CF947432	CF947432 UI-D-GC1-
C 247	37.6	1.6	902	29	CNS00CVM	AL060007 Drosophil	320	37	1.5	507	14	CD739626	CD739626 4028268 1
C 248	37.6	1.6	1028	13	BX376226	BX376226 BX376226	321	37	1.5	593	10	BE444849	BE444849 WHE1129 B
C 249	37.6	1.6	1101	29	CNS0039G	AL063921 Drosophil	322	37	1.5	726	13	BX306217	BX306217 BX306217
C 250	37.6	1.6	1131	9	AL517123	AL517123 AL517123	323	37	1.5	761	13	BU271162	BU271162 603814887
C 251	37.6	1.6	1638	10	BF137817	BF137817 601782464	324	37	1.5	850	29	CG240021	CG240021 OGD166TV
C 252	37.4	1.6	239	10	BF874262	BF874262 IL3-ET011	325	37	1.5	859	12	BI857846	BI857846 603388406
C 253	37.4	1.6	247	28	BZ851677	BZ851677 CH240 267	C 326	37	1.5	874	12	BG755301	BG755301 602714044
C 254	37.4	1.6	294	13	BQ836079	BQ836079 rf41e10.Y	C 327	37	1.5	884	13	BQ214135	BQ214135 AGENCOURT
255	37.4	1.6	322	10	AW114856	AW114856 rs60d04.Y	C 328	37	1.5	1004	29	CNS032TV	AL268060 Tetraodon
C 256	37.4	1.6	380	9	AI273765	AI273765 ql47h07.x	329	37	1.5	1061	13	BX391246	BX391246 BX391246
C 257	37.4	1.6	409	10	BF968022	BF968022 602269544	330	37	1.5	1067	10	BF797585	BF797585 602257382
C 258	37.4	1.6	410	14	WL2162	WL2162 ma62e12.r1	C 331	37	1.5	1109	29	AG129047	AG129047 Pan trogl
C 259	37.4	1.6	419	9	AI367917	AI367917 qk66c11.x	332	37	1.5	1201	9	AL565971	AL565971 AL565971
C 260	37.4	1.6	421	9	AI273323	AI273323 ql45e04.x	333	37	1.5	1201	13	BX360604	BX360604 BX360604
261	37.4	1.6	441	9	AA488481	AA488481 ab39a04.x	334	37	1.5	1201	13	BX442961	BX442961 BX442961
C 262	37.4	1.6	446	9	AI304808	AI304808 qo63e10.x	335	37	1.5	1201	13	BX444892	BX444892 BX444892
C 263	37.4	1.6	469	9	AI346735	AI346735 qp52e11.x	336	36.8	1.5	455	14	CB741917	CB741917 AMGNNUC:M
264	37.4	1.6	528	14	CB123677	CB123677 K-EST0172	337	36.8	1.5	530	29	CE794563	CE794563 tigr-gss-
265	37.4	1.6	535	12	BM846845	BM846845 K-EST0125	C 338	36.8	1.5	575	29	DR26M24T	AL973834 Danio rer
266	37.4	1.6	549	12	BM839796	BM839796 K-EST0116	C 339	36.8	1.5	625	29	BX189757	BX189757 Danio rer
267	37.4	1.6	575	10	BE257300	BE257300 601108507	C 340	36.8	1.5	632	28	AZ640745	AZ640745 1M0502K23
268	37.4	1.6	580	28	BH715317	BH715317 BOMAZ40TR	C 341	36.8	1.5	657	10	BB446136	BB446136 BB446136
269	37.4	1.6	616	10	BE252565	BE252565 601113414	C 342	36.8	1.5	673	12	BJ058651	BJ058651 BJ058651
C 270	37.4	1.6	645	28	BH575576	BH575576 BOGNOU04TR	C 343	36.8	1.5	861	12	BM416448	BM416448 OP21542 M
C 271	37.4	1.6	648	13	BX119057	BX119057 BX119057	C 344	36.8	1.5	912	12	BI103816	BI103816 602885678
272	37.4	1.6	680	12	BG491601	BG491601 602535928	C 345	36.8	1.5	2486	11	AK051015	AK051015 Mus muscu
273	37.4	1.6	692	29	CNS007WH	AL050923 Drosophil	C 346	36.6	1.5	394	29	CE213512	CE213512 tigr-gss-
274	37.4	1.6	702	10	BE253792	BE253792 601112617	C 347	36.6	1.5	465	14	CD848707	CD848707 DH0AC010Z
C 275	37.4	1.6	711	13	BX734048	BX734048 BX734048	C 348	36.6	1.5	529	13	BQ353960	BQ353960 PM0-HT091
C 276	37.4	1.6	715	14	CD348996	CD348996 UI-M-FY0-	C 349	36.6	1.5	644	13	BU813716	BU813716 N014C03 P
277	37.4	1.6	841	12	BI087131	BI087131 602850807	350	36.6	1.5	674	13	CA135098	CA135098 SCJLRT101
278	37.4	1.6	876	13	BQ644304	BQ644304 AGENCOURT	351	36.6	1.5	697	29	CE186464	CE186464 tigr-gss-
279	37.4	1.6	896	13	BU931047	BU931047 AGENCOURT	C 352	36.6	1.5	702	28	AQ448154	AQ448154 mgxb0017K
280	37.4	1.6	917	13	BQ889933	BQ889933 AGENCOURT	C 353	36.6	1.5	706	12	BM971661	BM971661 UI-CF-EC1
281	37.4	1.6	919	29	CNS00655	AL065856 Drosophil	C 354	36.6	1.5	736	13	BU130913	BU130913 603117145
282	37.4	1.6	926	13	BQ652379	BQ652379 AGENCOURT	355	36.6	1.5	762	13	CA088556	CA088556 SCRFAM212
283	37.4	1.6	929	13	BQ653104	BQ653104 AGENCOURT	C 356	36.6	1.5	838	14	CF289958	CF289958 AGENCOURT
284	37.4	1.6	937	13	BQ650376	BQ650376 AGENCOURT	357	36.6	1.5	884	10	BF569519	BF569519 602186015
285	37.4	1.6	939	13	BQ877227	BQ877227 AGENCOURT	358	36.6	1.5	948	28	CC368521	CC368521 PUHOW70TD
286	37.4	1.6	956	13	BQ651346	BQ651346 AGENCOURT	359	36.6	1.5	997	29	CNS005TE	AL060767 Drosophil
C 287	37.4	1.6	962	13	BX383763	BX383763 BX383763	C 360	36.6	1.5	1026	13	BX354717	BX354717 BX354717
288	37.4	1.6	1007	13	BQ056184	BQ056184 AGENCOURT	361	36.6	1.5	1068	9	AL527496	AL527496 AL527496
289	37.4	1.6	1021	12	BQ052974	BQ052974 AGENCOURT	C 362	36.6	1.5	1163	9	AL577643	AL577643 AL577643
290	37.4	1.6	1037	12	BM927940	BM927940 AGENCOURT	363	36.6	1.5	1201	9	AL513905	AL513905 AL513905
291	37.4	1.6	1045	12	BQ051836	BM051836 AGENCOURT	364	36.4	1.5	499	12	BM694274	BM694274 UI-E-C11-
292	37.4	1.6	1050	12	BM562665	BM562665 AGENCOURT	365	36.4	1.5	606	13	BU327441	BU327441 603495111
293	37.4	1.6	1088	12	BM928461	BM928461 AGENCOURT	366	36.4	1.5	647	12	BI392755	BI392755 ppg1n.pk0
294	37.4	1.6	1098	13	BQ876947	BQ876947 AGENCOURT	C 367	36.4	1.5	693	12	BJ505146	BJ505146 BJ505146
295	37.4	1.6	1217	12	BM906870	BM906870 AGENCOURT	C 368	36.4	1.5	727	28	BH012641	BH012641 TDGAM05TH
296	37.4	1.6	1227	12	BM913126	BM913126 AGENCOURT	C 369	36.4	1.5	729	29	CC587503	CC587503 CH240_385

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C 370	36.4	1.5	794	12	BG471870	BG471870	602513345	C 443	35.8	1.5	706	28	BZ805325	BZ805325	PUGV61TD
C 371	36.4	1.5	816	28	BH552486	BH552486	BOGXX72TF	444	35.8	1.5	707	11	AY110674	AY110674	Zea mays
C 372	36.4	1.5	833	28	BH440313	BH440313	BOGYE35TR	445	35.8	1.5	725	12	BG820612	BG820612	602780593
C 373	36.4	1.5	848	9	AL528948	AL528948	AL528948	446	35.8	1.5	833	28	CC415585	CC415585	PUEKB41TD
C 374	36.4	1.5	1040	13	BX375588	BX375588	BX375588	C 447	35.8	1.5	870	13	BU305820	BU305820	603611480
C 375	36.4	1.5	1179	13	BX403696	BX403696	BX403696	C 448	35.8	1.5	877	14	CD328705	CD328705	AGENCOURT
C 376	36.4	1.5	1203	29	CNS015Y4	AL106054	Drosophil	C 449	35.8	1.5	902	12	BM459710	BM459710	AGENCOURT
C 377	36.2	1.5	331	14	CF182006	CF182006	ISO5D2F I	C 450	35.8	1.5	912	29	CG278321	CG278321	OG2AE85TV
C 378	36.2	1.5	552	28	AZ085485	AZ085485	RPCI-23-4	C 451	35.8	1.5	946	29	CG094044	CG094044	PUIIO25TB
C 379	36.2	1.5	662	10	BE570838	BE570838	601329345	C 452	35.8	1.5	984	13	BX369944	BX369944	BX369944
C 380	36.2	1.5	796	13	BU263851	BU263851	603815664	453	35.8	1.5	990	29	AG041486	AG041486	Pan trogl
C 381	36.2	1.5	828	13	BU706990	BU706990	UI-M-FR0-	C 454	35.8	1.5	1041	29	AG042970	AG042970	Pan trogl
C 382	36.2	1.5	833	28	BZ971078	BZ971078	BZ971078	455	35.8	1.5	1064	9	AL549536	AL549536	AL549536
C 383	36.2	1.5	904	29	CNS00F2V	AL070170	Drosophil	456	35.8	1.5	1068	29	CNS01HUZ	AL144924	Anopheles
C 384	36.2	1.5	946	13	BX431296	BX431296	BX431296	457	35.8	1.5	1101	29	CNS016R4	AL107098	Drosophil
C 385	36.2	1.5	977	29	CNS00JX7	AL076850	Drosophil	458	35.8	1.5	1103	13	BX403654	BX403654	BX403654
C 386	36.2	1.5	1009	29	CNS010EW	AL098882	Drosophil	C 459	35.8	1.5	1200	13	BX339396	BX339396	BX339396
C 387	36.2	1.5	1073	13	BQ073722	BQ073722	AGENCOURT	460	35.8	1.5	3191	11	AF318370	AF318370	Homo sapi
C 388	36.2	1.5	1201	9	AL538546	AL538546	AL538546	461	35.6	1.5	367	12	BG273600	BG273600	OV2_27_F1
C 389	36.2	1.5	1201	13	BX394133	BX394133	BX394133	C 462	35.6	1.5	456	9	AL450697	AL450697	AL450697
C 390	36.2	1.5	1201	13	BX462261	BX462261	BX462261	C 463	35.6	1.5	505	14	CD859582	CD859582	G15_001L1
C 391	36	1.5	279	28	AQ583874	AQ583874	RPCI-11-4	C 464	35.6	1.5	528	28	AQ412180	AQ412180	RPCI-11-1
C 392	36	1.5	379	10	BE293358	BE293358	601143788	465	35.6	1.5	551	10	BE808235	BE808235	213389 MA
C 393	36	1.5	401	28	AQ456822	AQ456822	HS_5153 A	466	35.6	1.5	554	12	BG649430	BG649430	EM1_79 CI
C 394	36	1.5	422	28	AZ830739	AZ830739	2M0110H1	467	35.6	1.5	578	12	BG733185	BG733185	346924 MA
C 395	36	1.5	435	10	BB821911	BB821911	BB821911	468	35.6	1.5	616	14	CD207639	CD207639	HS1_33 E0
C 396	36	1.5	503	28	BZ940143	BZ940143	CH240_107	469	35.6	1.5	640	14	CF489420	CF489420	POL1_57 B
C 397	36	1.5	512	13	BQ552616	BQ552616	H4017A05-	470	35.6	1.5	644	14	CB346417	CB346417	CAB2SG000
C 398	36	1.5	541	14	CD694912	CD694912	EST11435	471	35.6	1.5	654	14	CD463636	CD463636	ETH1_45 E
C 399	36	1.5	566	28	BH788848	BH788848	fzmb021f0	472	35.6	1.5	670	13	BQ998962	BQ998962	OGG20L17.
C 400	36	1.5	568	12	BM072819	BM072819	MEST54-B0	473	35.6	1.5	678	9	AL855511	AL855511	AL855511
C 401	36	1.5	586	13	C88262	C88262	C88262	C 474	35.6	1.5	699	29	CG954192	CG954192	MBEIX80TF
C 402	36	1.5	596	14	CB604629	CB604629	Mous	475	35.6	1.5	701	12	BG535399	BG535399	602563060
C 403	36	1.5	624	12	BM379926	BM379926	MEST512-E	476	35.6	1.5	710	13	BQ750606	BQ750606	EST633342
C 404	36	1.5	635	14	CB380742	CB380742	3529_1_24	477	35.6	1.5	710	14	CF480132	CF480132	POL1_63 H
C 405	36	1.5	653	29	CC591764	CC591764	CH240_392	C 478	35.6	1.5	841	29	CG293401	CG293401	OGWFN35TH
C 406	36	1.5	666	10	AW267379	AW267379	829001F08	479	35.6	1.5	881	28	BH133926	BH133926	ENTNC94TF
C 407	36	1.5	669	13	BU380717	BU380717	603860438	480	35.6	1.5	885	13	BX425603	BX425603	EX425603
C 408	36	1.5	753	28	BH662058	BH662058	BOMMU12TF	C 481	35.6	1.5	894	29	CNS01591	AL105168	Drosophil
C 409	36	1.5	773	12	BI765770	BI765770	603046528	C 482	35.6	1.5	925	29	CNS0091P	AL053013	Drosophil
C 410	36	1.5	775	13	BU129977	BU129977	603118120	C 483	35.6	1.5	936	13	BX383396	BU123103	603148360
C 411	36	1.5	792	29	CG360302	CG360302	OGWJQ01TV	C 484	35.6	1.5	953	13	BQ889234	BX383396	EX383396
C 412	36	1.5	803	29	CG428158	CG428158	ZMMBBb023	C 485	35.6	1.5	1080	29	AG146549	BQ889234	AGENCOURT
C 413	36	1.5	804	28	BH180602	BH180602	017_1_21-	C 486	35.6	1.5	1101	29	CNS000C9	AG146549	Pan trogl
C 414	36	1.5	804	29	CNS07MF3	AL617553	T7_end of	C 487	35.6	1.5	1101	29	CNS000BMG	AL065386	Drosophil
C 415	36	1.5	805	28	BZ278574	BZ278574	CH230-308	C 488	35.6	1.5	1147	28	CC289353	AL057362	Drosophil
C 416	36	1.5	813	29	CG604153	CG604153	OGUHL30TV	C 489	35.6	1.5	1201	13	BX376097	CC289353	CH261-185
C 417	36	1.5	837	12	BG754193	BG754193	602709741	C 490	35.6	1.5	1201	13	BX443061	BX376097	EX376097
C 418	36	1.5	840	29	CC655714	CC655714	OGUKS21TH	C 491	35.6	1.5	1201	13	BX443061	BX443061	EX443061
C 419	36	1.5	867	29	CG047358	CG047358	PURSU09TD	C 492	35.6	1.5	1201	13	BX444397	BX444397	EX444397
C 420	36	1.5	902	28	BZ579707	BZ579707	msh2_733.	C 493	35.4	1.5	348	9	AI417728	AI417728	th26f05..x
C 421	36	1.5	909	29	CNS02POE	AL208247	Tetraodon	C 494	35.4	1.5	428	9	AI972798	AI972798	wr43G01.x
C 422	36	1.5	927	12	BI906112	BI906112	603062512	C 495	35.4	1.5	432	13	BQ309149	BQ309149	MR0-BT600
C 423	36	1.5	960	29	CG291153	CG291153	OG0CD02TV	496	35.4	1.5	479	10	AW769815	AW769815	hk53G10.x
C 424	36	1.5	982	13	BX415111	BX415111	BX415111	497	35.4	1.5	515	13	BX424977	BX424977	EX424977
C 425	36	1.5	1000	13	BX407619	BX407619	EX407619	498	35.4	1.5	540	13	CA018868	CA018868	HV09007x
C 426	36	1.5	1041	28	CC089026	CC089026	CSU-K33r.	499	35.4	1.5	542	28	AQ433365	AQ433365	HS_5050 B
C 427	36	1.5	1181	10	BF206810	BF206810	601870206	500	35.4	1.5	543	13	BU398335	BU398335	603534591
C 428	36	1.5	1201	9	AL530352	AL530352	AL530352								
C 429	36	1.5	1351	13	BQ955445	BQ955445	AGENCOURT								
C 430	36	1.5	3948	11	AK029787	AK029787	Mus muscu								
C 431	35.8	1.5	325	12	BM019568	BM019568	603647788								
C 432	35.8	1.5	339	29	CC772228	CC772228	CH240_801								
C 433	35.8	1.5	370	9	AA865012	AA865012	od49b11.s								
C 434	35.8	1.5	403	9	AA190879	AA190879	zp85c05.s								
C 435	35.8	1.5	448	9	AL372928	AL372928	McBA54E09								
C 436	35.8	1.5	448	10	BE552503	BE552503	946078A02								
C 437	35.8	1.5	448	14	CA871882	CA871882	K0913G12-								
C 438	35.8	1.5	473	13	BQ904708	BQ904708	Ta04_1090								
C 439	35.8	1.5	554	29	CNS042ID	AL271534	Tetraodon								
C 440	35.8	1.5	573	12	BM743673	BM743673	K-EST0016								
C 441	35.8	1.5	658	12	BJ253084	BJ253084	BJ253084								
C 442	35.8	1.5	678	29	BX129833	BX129833	Danio rer								

ALIGNMENTS

RESULT 1	BX377108	1201 bp	linear	EST 08-MAY-2003
LOCUS	BX377108	Homo sapiens	PLACENTA COT 25-NORMALIZED	Homo sapiens CDNA
DEFINITION	BX377108	clone CSODI002YE24	5-PRIME, mRNA sequence.	
ACCESSION	BX377108	GI:30442891		
VERSION	BX377108.1	EST.		
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jesse,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)

Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2614.f For more information about this cluster, see http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI002BC12QP1&cluster=2614.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DI002BC12QP1.

Location/Qualifiers 1..1201 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DI002YE24" /tissue_type="PLACENTA COT 25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 29.7%; Score 710.8; DB 13; Length 1201; Best Local Similarity 95.1%; Pred. No. 4.4e-190; Matches 750; Conservative 4; Mismatches 32; Indels 3; Gaps 2;

QY 1599 GTGCCAAGTGTGGCAGTGCCTGGACAGGGGGCTCAGGGAAGGACGTGGAGCAGCCTT 1658
Db 48 GTCGGGAATTCCTCCGGATGCCCTGGACAGGGGGCTCAGGGAAGGACGTGGAGCAGCCTT 107
QY 1659 ATCCAGGCCTCTGGGTGTCCCGACACAGGTGTTCACATCTGTGTGTCAGTTCAGATGC 1718
Db 108 ATCCAGGCCTCTGGGTGTCCCGACACAGGTGTTCACATCTGTGTGTCAGTTCAGATGC 167
QY 1719 CTCAGTTCCTGGAAAGCTAGGTTCTTCGCACTGTTCACCAAGGTGATTGTAAGAGCTGGC 1778
Db 168 CTCAGTTCCTGGAAAGCTAGGTTCTTCGCACTGTTCACCAAGGTGATTGTAAGAGCTGGC 227
QY 1779 GGTACACAGAGAACAGCCCCCAGCTGAGGGGGTGTGTGAAT--CGGACAGCCTCCCAG 1836
Db 228 GGTACACAGAGAACAGCCCCCAGCTGAGGGGGTGTGTGAATTCGACAGGCCTCCCAG 287
QY 1837 CAGAGGTGTGGAGCTGCAGCTGAGGGAAGAGACAAATCGGCCCTGGACACTCAGGAGG 1896
Db 288 CAGAGGTGTGGAGCTGCAGCTGAGGGAAGAGACAAATCGGCCCTGGACACTCAGGAGG 347
QY 1897 GTCAAAAGGAGACTTGGTCGCACCACTCATCTGCCACCCCAAGATGCATCCTGCCTCA 1956
Db 348 GTCAAAAGGAGACTTGGTCGCACCACTCATCTGCCACCCCAAGATGCATCCTGCCTCA 407
QY 1957 TCAGGTCCAGATTTCTTTCCAGGCGGACGTTTCTGTGTGAATTCCTAGTCCCTGGCCT 2016
Db 408 TCAGGTCCAGATTTCTTTCCAGGCGGACGTTTCTGTGTGAATTCCTAGTCCCTGGCCT 467
QY 2017 CGGACACCTTCATTCGTTAGTGGGGAGTGGTGGTGGAGCAGTGAAGAGAGCGGATGG 2076
Db 468 CGGACACCTTCATTCGTTAGTGGGGAGTGGTGGTGGAGCAGTGAAGAGAGCGGATGG 527
QY 2077 TCACACTCAGATCCACAGAGCCAGGATCAAGGGACCACTGCAGTGGCAGCAGACTGT 2136
Db 528 TCACACTCAGATCCACAGAGCCAGGATCAAGGGACCACTGCAGT-GCAGGAGGACTGT 586
QY 2137 TGGGCCCCCAACCCCTGCACAGCCCTCATCCCTCTTGGCTTGAGCCGTGAGAGGC 2196

Db 587 TGGGCCCCCACCCCAACCCCTGCACAGCCCTCATCCCTCTTGGCTTGAGCCGTGAGAGC 646
QY 2197 CCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTTTGTTCATCAGGGCAGGCTTCCTC 2256
Db 647 CCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTTTGTTCATCAGGGCAGGCTTCCTC 706
QY 2257 GGAGCCAGGATGATCTGTGCCACGCTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTC 2316
Db 707 GGAGCCAGGATGATCTGTGCCACGCTTGACCTCGGGCCCATCTGGGCTCATGCGCGC 766
QY 2317 TCCTGCTATTGAATTAGTACCTAGCTGCACAGTATGTAGTTACCAAAAGATAAACGG 2376
Db 767 GYCTGCGATTGATTAGTACCTAGCTGCACACAKATGKTATTTACCAAAAGAWAAAAACGG 826
QY 2377 CAATAATTG 2385
Db 827 CATATTTTG 835

RESULT 2 CA308767/c
LOCUS CA308767 723 bp mRNA linear EST 01-NOV-2002
DEFINITION UI-H-FTI-bhy-b-03-0-UI.s1 NCI CGAP_FTI Homo sapiens cDNA clone UI-H-FTI-bhy-b-03-0-UI 3', mRNA sequence.
ACCESSION CA308767
VERSION CA308767.1 GI:24471821
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 723)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

Location/Qualifiers 1..723 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="UI-H-FTI-bhy-b-03-0-UI" /tissue_type="Alveolar Macrophage" /dev_stage="Adult" /lab_host="DH10B (Life Technologies)" /clone_lib="NCI CGAP FTI" /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI-CGAP FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dr)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

Tumor Gene Index

JOURNAL COMMENT

TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG

ORIGIN

Query Match 29.5%; Score 706.4; DB 14; Length 723;
Best Local Similarity 99.2%; Pred. No. 6.3e-189;
Matches 710; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1680 CGACACAGGTGTTACATCTGTGTGTCAGGTGAGTGCCTCAGTTCTTGGAAAGCTAGG 1739
Db |||||
QY 1740 TTCCTGCGACTGTTACCAAGGTGATTGTAAGAGCTGGCGGTACAGAGGAACAAGCCCC 1799
Db |||||
QY 1800 CCAGCTGAGGGGTGTGTAATCGGACAGCCTCCAGCAGAGGTGTGGAGCTGCAGCTG 1859
Db |||||
QY 1860 AGGGAAGAAGAGACAATCGGCTTGACACTCAGGAGGTCAAAGGAGACTTGGTCCGAC 1919
Db |||||
QY 1920 CACTCATCTGCCACCCCAAGATGATGTCCTCATCAGGTCCAGATTCTTTCCAAG 1979
Db |||||
QY 1980 GCGGACGTTTCTGTTGGAATCTTAGTCTCTGGCTCGGACACCTTCATTCGTTAGCTG 2039
Db |||||
QY 2040 GGGAGTGGTGAAGAGAGAGGCGGATGTCACACTCAGATCCACAGAGCCC 2099
Db |||||
QY 2100 AGGATCAAGGACCCACTGCGAGTGGCAGGACTGTTGGGCCCCCAACCCCTGCG 2159
Db |||||
QY 2160 CAGCCCTCATCCCTCTTGGCTGAGCCGTCAGAGGCCCTGTGCTGAGTGTCTGACCGAG 2219
Db |||||
QY 2220 ACACCTCACAGCTTGTGTCATCAGGACAGGCTTCTCGGAGCCAGGATGATCTGTGCCAC 2279
Db |||||
QY 2280 GCTTGACCTCGGCCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTA 2339
Db |||||
QY 2340 GCTGCACACAGTATGTAGTTACCAAGAATAAACGGCAATAATTGAGAAAAAAA 2395
Db |||||

RESULT 3
BU622377/c
LOCUS
DEFINITION
UI-H-FL1-bfz-c-21-0-UI.s1 NCI CGAP_FLI1 Homo sapiens cDNA clone
UI-H-FL1-bfz-c-21-0-UI 3', mRNA sequence.
ACCESSION
BU622377
VERSION
BU622377.1 GI:23288592
KEYWORDS
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 731)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES source

Location/Qualifiers
1..731
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FL1-bfz-c-21-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_FLI1"
/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP_FLI1 is a normalized cDNA library derived from a pool of mRNA obtained from 4 cell lines from grade III chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dT)18 tail. The sequence tag for this library is GAGGTCCGTC. The cell lines were provided by Dr. James Martin from the University of Iowa.
TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
TAG_LIB=UI-H-FL1
TAG_SEQ=GAGGTCCGTCG"

ORIGIN

Query Match 29.4%; Score 704.6; DB 13; Length 731;
Best Local Similarity 99.3%; Pred. No. 2e-188;
Matches 718; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1674 GTGTCCCGACACAGGTGTTACATCTGTGTGTCAGGTGATGCCTCAGTTCTTGGAAA 1733
Db |||||
QY 1734 GCTAGGTTCTCGACTGTTACCAA-CGTGATTGTAAAGAGCTGGCGGTACAGAGGAAC 1792
Db |||||
QY 1793 AAGCCCCCAGCTGAGGGGTGTGTGAATCGGACAGCCTCCCAGCAGAGGTGTGGAGCT 1852
Db |||||
QY 1853 GCAGCTGAGGGAAGAAGAGACAATCGGCTTGACACTCAGGAGGTCAAAGGAGACTTG 1912
Db |||||
QY 1913 GTCGACCACTCATCTGCCACCCCGAGAAATCGCTGCCTCATCAGGTCCAGATTCT 1972
Db |||||
QY 1973 TTCCAAGGCGGACGTTTCTGTTGGAATTTCTAGTCTCTGGCCTCGGACACCTTCATCG 2032
Db |||||
QY 2033 TTAGCTGGGAGTGGTGGTGGAGCAGTGAAGAAGAGCGGAGTGGTCACTCAGATCCAC 2092
Db |||||

Fri Aug 6 10:49:40 2004

JOURNAL
COMMENT

Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM613 row: f column: 21
High quality sequence stop: 628.
Location/Qualifiers

FEATURES
source

1. .825
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/clone="IMAGE:30528044"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 147"
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all-XhoI; Site 2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTNN-3', size-selected for average
insert size 2.3 kb and normalized to 10^5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NHGRI/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."

ORIGIN

Query Match 28.5%; Score 682.6; DB 14; Length 825;
Best Local Similarity 95.9%; Pred. No. 3.9e-182;
Matches 722; Conservative 0; Mismatches 29; Indels 2; Gaps 2;
QY 1 CCTGGAGCCGGAAGCGCGCTGCAGCAGGGCGAGGCTCCAGGTGGGTTCGGTCCGCATC 60
DB 66 CCTGGAGCCGGAAGCGCGCTGCAGCAGGGCGAGGCTCCAGGTGGGTTCGGTCCGCATC 125
QY 61 CAGCCTAGCGTCCACGATCGCGGTGGGTCCGGGACTTCCTCCGGCTCCCGTTCGTTCCG 120
DB 126 CAGCCTAGCGTCCACGATCGCGGTGGGTCCGGGACTTCCTCCGGCTCCCGTTCGTTCCG 185
QY 121 ATCGAGGTGCTAGGATCGCGGTTCCTTCGGGGATTCCTCCGGCTCCCGTTCGTTCC 180
DB 186 ATCGAGGTGCTAGGATCGCGGTTCCTTCGGGGATTCCTCCGGCTCCCGTTCGTTCC 245
QY 181 TCTGCAGAGCGGAACACGAGCGGAGCCCCAGCGCCCGGAGCCCTCGGCTGGAGCCAGT 240
DB 246 TCTGCAGAGCGGAACACGAGCGGAGCCCCAGCGCCCGGAGCCCTCGGCTGGAGCCAGT 305
QY 241 TCTAAGTGCAGCAGCTGCCACCCCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGAT 300
DB 306 TCTAAGTGCAGCAGCTGCCACCCCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGAT 365
QY 301 GCCTTGAGAGATGATTTGTGTTGGGTCAAAGGGTGTGAATTTATGCCCTACACAAC 360
DB 366 GCCTTGAGAGATGATTTGTGTTGGGTCAAAGGGTGTGAATTTATGCCCTACACAAC 425
QY 361 TACCTTGTGGAAGGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT 420
DB 426 TACCTTGTGGAAGGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT 485
QY 421 ACTATGCCTCGAATCAAGGATTTGATGACGGGAGCCTTCCTGGCTTTGTGCGACGTCATC 480
DB 486 ACTATGCCTCGAATCAAGGATTTGATGACGGGAGCCTTCCTGGCTTTGTGCGACGTCATC 545
QY 481 AGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAGCAGCT 540

Db 546 AGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAGCAGCT 605
QY 541 GGAAAAAGAAATAGTCTTTTATGAGATGAACCTGGTGGTTAAATATTATCCAAAGCATTTT 600
DB 606 GGAAAAAGAAATAGTCTTTTATGAGATGAACCTGGTGGTTAAATATTATCCAAAGCATTTT 665
QY 601 GTGGAATATGATGGAACAACTCATTTTTCGTGTGAGATTACACAGAGGTGGATAATAAT 660
DB 666 GTGGAATATGATGGAACAACTCATTTTTCGTGTGAGATTACACAGAGGTGGATAATAAT 725
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DB 726 GTCACGAGGCAATTGGATAAAGTATTAAAAAGAGGAGATTGGGGACATATTATTAATCC 785
QY 719 ACTACCTGGGGCTGGACCAACATTTGGCCACATTT 751
DB 786 TTCACCTACCTGGGGCCTGGGACCCACATTT 818

RESULT 6
BG171457

LOCUS 602321972F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4425448 5',
DEFINITION mRNA sequence.
ACCESSION BG171457
VERSION BG171457.1 GI:12678160
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 809)
JOURNAL NIH-MGC http://mgi.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10170 row: o column: 17
High quality sequence stop: 653.
Location/Qualifiers

FEATURES
source

1. .809
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/clone="IMAGE:4425448"
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/lab_host="DH10B (phage-resistant)"
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 27.6%; Score 662.2; DB 12; Length 809;
Best Local Similarity 95.7%; Pred. No. 2.4e-176;
Matches 734; Conservative 0; Mismatches 28; Indels 5; Gaps 5;
QY 173 TTCGTTCTCTGCGAGCGGAACACCGGA-GCGGAGCCCCCAGCGCCGACCCCTCG-GC 230
DB 1 TTCGTTCTCTGCGAGCGGAACACCGGACGCGGAGCCCCCAGCGCCGACCCCTCGTC 60
QY 231 TGGAGCCAGTTCTAACTGGACCAACGCTGCCACCACTCTCTTCAGTAAAGTTGTTATGT 290

Db 61 TGGAGCCAGTTCTAACTGGACCAAGCTGCCACACCTCTCTTCAGTAAAGTTGTATTGT 120

QY 291 TCTGATAGATGCTTGGAGAGATGATTTTGTGTTTGGGTCAAAGGTTGTAATTTATGCC 350

Db 121 TCTGATAGATGCTTGGAGAGATGATTTTGTGTTTGGGTCAAAGGTTGTAATTTATGCC 180

QY 351 CTACACAACTTACCTTGTGGAAAAAGGAGCATCTCACAGTTTGTGGTGAAGCAAGCC 410

Db 181 CTACACAACTTACCTTGTGGAAAAAGGAGCATCTCACAGTTTGTGGTGAAGCAAGCC 240

QY 411 ACCTACAGTTACTATGCCTCGAATCAAGSCATTTGATGACGGGGAGCCTTCTGGCTTTGT 470

Db 241 ACCTACAGTTACTATGCCTCGAATCAAGSCATTTGATGACGGGGAGCCTTCTGGCTTTGT 300

QY 471 CGACGTCATCAGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGCAAGC 530

Db 301 CGACGTCATCAGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGCAAGC 360

QY 531 AAAAGCAGCTGGAAGAAAGATAGTCTTTTATGGAGATGAACCTGGGTTAAATTTATCCC 590

Db 361 AAAAGCAGCTGGAAGAAAGATAGTCTTTTATGGAGATGAACCTGGGTTAAATTTATCCC 420

QY 591 AAAGCATTTTGTGGAATATGATGGAACCAACCTCAATTTTCTGTGTCAGATTACACAGAGT 650

Db 421 AAAGCATTTTGTGGAATATGATGGAACCAACCTCAATTTTCTGTGTCAGATTACACAGAGT 480

QY 651 GGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAGAGAGGAGATTGGGACATATT 710

Db 481 GGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAGAGAGGAGATTGGGACATATT 540

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Db 541 AATCCTCCACTACCTGGGGCTGGACCACATTTGGCCACATTTTCCAGGGCCCAACAGCCCTT 600

QY 771 GATTGGGCAGAGCTGACGAGATGGACAGCGTGTGATGAAGATCCACACTCACTGCA 830

Db 601 GATTGGGCAGAGCTGACGAGATGGACAGCGTGTGATGAAGATCCACA-CTCACTGCA 659

QY 831 GTCGAAGGAG-AGAGAGACGCTTTACCCAAATTTGCTGTTCTTTG-TGCTGACCATGGC 888

Db 660 GTCGAAGAGAGAGAGAGCGCTTTTACCCAAATTTGCTGTTCTTTGCTGCTGAACATGGC 719

QY 889 ATGCTGTAACAGGAAGTACAGGGGCTCTCTCCACCGAGGAGGTGAA 935

Db 720 TTGTTTGCAACGGCCGTCCCGGGCTCTCCAGGAAGGAGTTGAATAA 766

RESULT 7
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LOCUS
DEFINITION
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BU191836
BU191836.1 GI:22705820
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 905)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1322 row: o column: 02

FEATURES
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High quality sequence stop: 656.
Location/Qualifiers
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/organism="Homo sapiens"
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/clone="IMAGE:6019801"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_70"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.1 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 27.4%; Score 655.6; DB 13; Length 905;
Best Local Similarity 96.3%; Pred. No. 1.9e-174;
Matches 704; Conservative 0; Mismatches 20; Indels 7; Gaps 3;
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Db 1 TACACAGAGGTGGATAATAATGTCAAGGCGCATTTGGATAAAGTATTAAGAGGAGAT 60
QY 700 TGGACATATTATCCTCCACTACCTGGGGCTGGACCACATTTGCCACATTTTCAGGGCCC 759
Db 61 TGGACATATTATCCTCCACTACCTGGGGCTGGACCACATTTGCCACATTTTCAGGGCCC 120
QY 760 AACAGCCCCCTGATTGGGCAGAAAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCAC 819
Db 121 AACAGCCCCCTGATTGGGCAGAAAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCAC 180
QY 820 ACCTCACTGAGTCGAAAGGAGAGAGAGACGCGCTTTACCCAAATTTGCTGGTCTTTGTGGT 879
Db 181 ACCTCACTGAGTCGAAAGGAGAGAGAGACGCGCTTTACCCAAATTTGCTGGTCTTTGTGGT 240
QY 880 GACCATGGCATGCTGAAACAGGAAGTCAAGGGGCTCTCCACCGAGGAGGTGAATACA 939
Db 241 GACCATGGCATGCTGAAACAGGAAGTCAAGGGGCTCTCCACCGAGGAGGTGAATACA 300
QY 940 CCTCTGATTTTAAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACATCCAAAG 999
Db 301 CCTCTGATTTTAAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACATCCAAAG 360
QY 1000 CACGTCCAATAGACGGATGTGGTGGACACTGGCGATAGCACTTGGCTTACCGATTCCA 1059
Db 361 CACGTCCAATAGACGGATGTGGTGGACACTGGCGATAGCACTTGGCTTACCGATTCCA 420
QY 1060 AAAGACAGTGTAGGAGCCCTCTATTCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAG 1119
Db 421 AAAGACAGTGTAGGAGCCCTCTATTCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAG 480
QY 1120 TTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCCG 1179
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Db 541 TCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTGCAAAAGATTGCTGGGAAC 600
QY 1240 TGGATCAGACTGTACTTGGAGGAAAGCATTCAGAGTCTTATCAACCTGGCTCCAAG 1299
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QY 1300 GTTCTC---AGGCAGTACCTGGATGCTCT---GAAGACGCTGAGCTT-GTCCCTGAGTGC 1352
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QY 1353 ACAAGTGGGCC 1363
Db 721 ACAAGTGGGCC 731

Fri Aug 6 10:49:40 2004

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RESULT 8
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LOCUS
DEFINITION
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IMAGE:30531017 5', mRNA sequence.
CF593551
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 971)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs@mail.nih.gov
Tissue procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM621 row: b column: 18
High quality sequence stop: 651.
Location/Qualifiers
1. .971
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/mol_type="mRNA"
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/clone="IMAGE:30531017"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-XhoI; Site_2: BamHI; Oligo-dT primed using primer
5'-TTTTTTTCTTTTCTTTT-3', size-selected for average
insert size 2.3 kb and normalized to 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."
ORIGIN
Query Match 27.0%; Score 646.4; DB 14; Length 971;
Best Local Similarity 99.8%; Pred. No. 8.3e-172;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCTGGAGCCGGAAGCGCGCTGCAGCAGGCGGAGGCTCCAGTGGGGTCCGGTCCGCATC 60
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QY 44 CCTGGAGCCGGAAGCGCGCTGCAGCAGGCGGAGGCTCCAGTGGGGTCCGGTCCGCATC 103
Db |||||||
QY 61 CAGCCTAGCGTGTCCACGATCGGCTGGCTCCGGGACTTTCGCTACCTGTTCGTAGCG 120
Db |||||||
QY 104 CAGCCTAGCGTGTCCACGATCGGCTGGCTCCGGGACTTTCGCTACCTGTTCGTAGCG 163
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QY 121 ATCGAGGTGTAGGATCGCGTCTTCCTTCGGGATTCTTCCCGGCTCCCGTTCGTTCC 180
Db |||||||
QY 164 ATCGAGGTGTAGGATCGCGTCTTCCTTCGGGATTCTTCCCGGCTCCCGTTCGTTCC 223
Db |||||||
QY 181 TCTGCCAGAGCGGAACACGAGCGGAGCCGCCAGCCCGGAGCCCTCGGTCGGAGCCAGT 240
Db |||||||
QY 224 TCTGCCAGAGCGGAGACGAGCGGAGCCGCCAGCCCGGAGCCCTCGGTCGGAGCCAGT 283
Db |||||||
QY 241 TCTAACTGGACCGCTGCCACCACTCTCTTCTAGTAAAGTTGTTATTTCTGTATAGAT 300
Db |||||||
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284 TCTAACTGGACCGCTGCCACCACTCTCTTCTAGTAAAGTTGTTATTTCTGTATAGAT 343
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301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGGGTGAAATTTATGCCCTACACAAC 360
Db |||||||
344 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGGGTGAAATTTATGCCCTACACAAC 403
QY |||||||
361 TACCTTGTGGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAAGCCACCTACAG 420
Db |||||||
404 TACCTTGTGGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAAGCCACCTACAG 463
QY |||||||
421 ACTATGCCTCGAATCAAGGCATTGATGACGGGGAGCCTTCCCTGGCTTGTGACGTCATC 480
Db |||||||
464 ACTATGCCTCGAATCAAGGCATTGATGACGGGGAGCCTTCCCTGGCTTGTGACGTCATC 523
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481 AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGCAAGCAAAAGCAGCT 540
Db |||||||
524 AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGCAAGCAAAAGCAGCT 583
QY |||||||
541 GGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTTAAATTTCCCAAGCATT 600
Db |||||||
584 GGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTTAAATTTCCCAAGCATT 643
QY |||||||
601 GTGGAATATGATGGAACCACTCATTTTTCGTGTCAGATTACACAGAG 648
Db |||||||
644 GTGGAATATGATGGAACCACTCATTTTTCGTGTCAGATTACACAGAG 691
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RESULT 9
BQ001548/c
LOCUS
DEFINITION
UI-H-DH1-awr-e-06-0-UI.s1 NCI_CGAP_DH1 Homo sapiens cDNA clone
IMAGE:5893229 3', mRNA sequence.

ACCESSION
BQ001548
VERSION
BQ001548.1 GI:19726448
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 585)
REFERENCE
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
TITLE
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
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Location/Qualifiers
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_DH1 is a normalized cDNA library containing the
following tissue(s): VS-8 Cell line from Metastatic
Chondrosarcoma in Lung. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested

with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dr)18 tail. The sequence tag for this library is AGATCATTCG.

TAG_TISSUE=lung
TAG_LIB=UI-H-DH1
TAG_SEQ=AGATCATTCG

ORIGIN

Query Match		23.3%;	Score 557.2;	DB 12;	Length 585;
Best Local Similarity		98.6%;	Pred. No. 1.5e-146;		
Matches 562;		Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;
QY	1826	CAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAGAGACAATCGGCCTGGA	1885		
Db	585	CAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAGAGACAATCGGCCTGGA	526		
QY	1886	CACCTCAGGAGGTCAAAAGGAGACTTGGTCGCCACCACTCATCTGCCACCCCGAGATGC	1945		
Db	525	CACCTCAGGAGGTCAAAAGGAGACTTGGTCGCCACCACTCATCTGCCACCCCGAGATGC	466		
QY	1946	ATCCTGCCTCATCAGGTCAGATTCTTTCCAAAGCGGACGTTTCTGTGGAATCTTA	2005		
Db	465	ATCCTGCCTCATCAGGTCAGATTCTTTCCAAAGCGGACGTTTCTGTGGAATCTTA	406		
QY	2006	GTCCTTGGCCTCGGACACCTTCATTCGTTAGCTGGGAGTGGTGAGGAGTGAAGAA	2065		
Db	405	GTCCTTGGCCTCGGACACCTTCATTCGTTAGCTGGGAGTGGTGAGGAGTGAAGAA	346		
QY	2066	GAGGCGGATGGTCACACTCAGATCCACAGAGCCCGAGGATCAAGGACCCACTGCAGTGGC	2125		
Db	345	GAGGCGGATGGTCACACTCAGATCCACAGAGCCCGAGGATCAAGGACCCACTGCAGTGGC	286		
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Db	285	AGCAGGACTGTGGGCCCCCCCCACCCCAACCCCTGCACAGCCCTCATCCCTCTTGGCTTGAG	226		
QY	2186	CCGTGAGGCCCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTTTGTCTATCAGGGCA	2245		
Db	225	CCGTGAGGCCCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTTTGTCTATCAGGGCA	166		
QY	2246	CAGGCTCTCTCGGAGCCAGGATGATCTGTGCCACGCTTGACACCTCGGGCCCCATCTGGGCT	2305		
Db	165	CAGGCTCTCTCGGAGCCAGGATGATCTGTGCCACGCTTGACACCTCGGGCCCCATCTGGGCT	106		
QY	2306	CATGCTCTCTCTCCTGCTATTGAATAGTACCTAGCTGCACACAGTATGTAGTTACCAA	2365		
Db	105	CATGCTCTCTCTCCTGCTATTGAATAGTACCTAGCTGCACGAGTATGTAGTTACCAA	46		
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RESULT 10	AL703949	LOCUS	615 bp	mRNA	linear	EST 04-SEP-2003
DEFINITION DKFZp686F1428_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone						
ACCESSION AL703949						
VERSION AL703949.1 GI:19687304						
KEYWORDS EST.						
SOURCE Homo sapiens (human)						
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE 1 (bases 1 to 615)						
AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,W., Mewes,H.W., Weil,B. and Wiemann,S.						
TITLE EST (Ottenwaelder,B., Obermaier,B., Mewes,H.W., Weil,B. and Wiemann,S.)						
JOURNAL Unpublished (2001)						

COMMENT

Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequence available.
This clone (DKFZp686F1428) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..615
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/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

FEATURES

source

ORIGIN

Query Match		23.1%;	Score 554.2;	DB 9;	Length 615;
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QY	230	CTGGAGCCAGTCTTAACCTGGACCAACGCTGCCACCACTCTCTTCAAGTAAAGTTGTTATG	289		
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QY	350	CCTACACAACTTACCTTGTGGAAGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAGC	409		
Db	177	CCTACACAACTTACCTTGTGGAAGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAGC	236		
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Db	237	CACCTACAGTTACTATGCCTCGAATCAAGGCATTCATGACGGGAGCCTTCCTGGCTTTG	296		
QY	470	TCGACCTCATCAGGAACCTCAATTCTCCTGCACCTGCTGGAAGACAGTGTGATAAGACAAG	529		
Db	297	TCGACCTCATCAGGAACCTCAATTCTCCTGCACCTGCTGGAAGACAGTGTGATAAGACAAG	356		
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Db	357	CAAAAGCAGCTGGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTAAATTTATCC	416		
QY	590	CAAAGCATTTTGTGGATATGATGGAACAACCTCAATTTTCGTGTGAGATTACACAGAGG	649		
Db	417	CAAAGCATTTTGTGGATATGATGGAACAACCTCAATTTTCGTGTGAGATTACACAGAGG	476		
QY	650	TGGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAGAGAGGAGATTGGACATAT	709		
Db	477	TGGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAGAGAGGAGATTGGACATAT	536		
QY	710	TAATCTCCACTACCTGGGGCTGGACCACTTGGCCACATTTCAGGGCCCAACAGCCCCC	769		
Db	537	TAATCTCCACTACCTGGGGCTGGACCACTTGGCCACATTTCAGGGCCCAACAGCCCCC	596		
QY	770	TGATTGGCAGAAAGCTGAG	788		
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RESULT 11
BG742889
LOCUS

BG742889

801 bp

mRNA

linear

EST 15-MAY-2001

Fri Aug 6 10:49:40 2004

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QY	1615	GTGCCCTGGACAGGGGCTCAGGGAAGGACGCTGGAGCAGCCTTATCCAGGCCTCTGGG	1674
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QY	1794	AGCCCCCAGCTGA-GGGGGTGTGTGAATCGGACAGCCTCCAGCAGAGGTGTGGGAGCT	1852
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RESULT 13
CD517899
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VERSION
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
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IMAGE:30397358 5', mRNA sequence.
CD517899
CD517899.1 GI:31449617
EST.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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(Invitrogen). Note: this is a NIH_MGC Library."

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82.0%; Pred. No. 2.3e-118;

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RESULT 14

AL698226

LOCUS AL698226 546 bp mrna linear EST 04-SEP-2003

DEFINITION DKFZp686D11107_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686D11107_5' mRNA sequence.

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZp686D11107) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.

FEATURES

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2187	CGTCAGAGGCCCTGTGCTGAGTGTCTGACCGAGACACTCAGACTTTGTTCATCAGGGCAC	2246		
201	CGTCAGAGGCCCTGTGCTGAGTGTCTGTCGAGACACTCAGACTTTGTTCATCAGGGCAC	142		
2247	AGGCTTCTCGGAGCCAGGATGATCTGTGCCACGTTTGACCTCGGGCCCATCTGGGCTC	2306		
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2307	ATGCTCTCTCTCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTAGTTACAAAA	2366		

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 5, 2004, 15:44:49 ; Search time 9284 Seconds
(without alignments)
11181.233 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

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- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2395	100.0	2395	6	AX055478	AX055478 Sequence
2	2395	100.0	2395	6	AX089946	AX089946 Sequence
3	2395	100.0	2395	6	AX092408	AX092408 Sequence
4	2395	100.0	2395	6	AX358864	AX358864 Sequence
5	2395	100.0	2395	6	AX362357	AX362357 Sequence
6	2395	100.0	2395	6	AX454706	AX454706 Sequence
7	2395	100.0	2395	6	AX491184	AX491184 Sequence
8	2395	100.0	2395	6	AY358538	AY358538 Homo sapi
9	1922.8	80.3	3151	9	BC050262	BC050262 Homo sapi
10	1719.4	71.8	2630	6	AX834645	AX834645 Sequence
11	1719.4	71.8	2630	9	AK097244	AK097244 Homo sapi
12	1521.2	63.5	3197	6	BD127295	BD127295 Primer fo
13	1521.2	63.5	3197	9	AK074815	AK074815 Homo sapi
14	1266.6	52.9	3019	6	BD127743	BD127743 Primer fo
15	1266.6	52.9	3019	9	AK074715	AK074715 Homo sapi
16	992.2	41.4	2755	6	AX405871	AX405871 Sequence
17	849.2	35.5	97217	9	AC116565	AC116565 Homo sapi
18	824	34.4	857	6	BD126357	BD126357 Primer fo
19	785.2	32.8	1827	9	AB050262	AB050262 Macaca fa
20	731.6	30.5	818	6	BD124800	BD124800 Primer fo
21	731.6	30.5	818	6	BD126632	BD126632 Primer fo
22	558.8	23.3	2266	9	BC001249	BC001249 Homo sapi
23	510.4	21.3	566	6	BD124901	BD124901 Primer fo
24	510.4	21.3	566	6	BD126970	BD126970 Primer fo
25	324.4	13.5	2039	9	AK000272	AK000272 Homo sapi
26	277.4	11.6	801	6	AX867296	AX867296 Sequence
27	277.4	11.6	801	6	BD147358	BD147358 Primer fo
28	277.4	11.6	1966	6	AX876310	AX876310 Sequence
29	277.4	11.6	1966	6	BD156062	BD156062 Primer fo
30	277.4	11.6	1966	9	AK027465	AK027465 Homo sapi
31	233	9.7	144117	9	AC092574	AC092574 Homo sapi
32	213.8	8.9	3537	9	AK124537	AK124537 Homo sapi
33	175.6	7.3	185043	2	AC145604	AC145604 Mus muscu
34	175.6	7.3	193102	2	AC124107	AC124107 Mus muscu
35	175.6	7.3	214250	2	AC103314	AC103314 Rattus no
36	175.6	7.3	217036	2	AC122636	AC122636 Rattus no
37	175.6	7.3	264320	2	AC129100	AC129100 Rattus no
38	175.6	7.3	266098	2	AC099280	AC099280 Rattus no
39	166	6.9	331039	3	AC116988	AC116988 Dictyoste
40	147.8	6.2	225153	2	AC130757	AC130757 Rattus no
41	135.8	5.7	33481	8	SPAC13G6	Z54308 S.pombe chr
42	124.2	5.2	185043	2	AC145604	AC145604 Mus muscu
43	120.2	5.0	24032	3	CEF28C6	Z68315 Caenorhabdi
44	101.8	4.3	3352	9	BC029271	BC029271 Homo sapi
45	101.8	4.3	3671	6	AX376198	AX376198 Sequence
46	101.8	4.3	3671	6	AX697033	AX697033 Sequence
47	101.8	4.3	3671	9	AY358472	AY358472 Homo sapi
48	101.8	4.3	4109	9	HSM805160	AL8333956 Homo sapi
49	101.8	4.3	6655	9	AK090433	AK090433 Homo sapi
50	100.2	4.2	3959	8	AF321466	AF321466 Yarrowia
51	99.6	4.2	3053	8	AK068119	AK068119 Oryza sat
52	99.4	4.2	4400	8	AF348498	AF348498 Candida a
53	90.6	3.8	3531	10	BC036977	BC036977 Mus muscu
54	90.6	3.8	4254	10	AB038560	AB038560 Mus muscu
55	78.4	3.3	2918	3	AY069051	AY069051 Drosophil
56	78.4	3.3	50089	3	AC005641	AC005641 Drosophil
57	78.4	3.3	61550	2	AC019919	AC019919 Drosophil
58	78.4	3.3	78174	3	AC004280	AC004280 Drosophil
59	78.4	3.3	175285	3	AC008259	AC008259 Drosophil
60	78.4	3.3	184079	3	AC008258	AC008258 Drosophil
61	78.4	3.3	272100	3	AE003840	AE003840 Drosophil
62	73.6	3.1	3540	8	SCYJL062W	Z49337 S.cerevisia
63	73.6	3.1	17137	8	SCXCDNA	Z34288 S.cerevisia
64	66.4	2.8	38784	2	AC014012	AC014012 Drosophil
65	66.4	2.8	166160	3	AC011072	AC011072 Drosophil

66	66.4	2.8	316961	3	AE003799	AE003799 Drosophila	c 139	39.6	1.7	130878	9	AL450063	AL450063 Human DNA
67	63.6	2.7	205429	2	AC005506	AC005506 Plasmodium	c 140	39.6	1.7	167218	2	AC069041	AC069041 Homo sapi
68	63.6	2.7	253132	3	AE014846	AE014846 Plasmodium	c 141	39.6	1.7	179028	2	AC027046	AC027046 Homo sapi
69	63	2.6	3569	3	BT009934	BT009934 Drosophila	c 142	39.6	1.7	228436	2	AC113100	AC113100 Mus muscu
70	62.2	2.6	35030	8	SPBC27B12	AL021766 S.pombe c	c 143	39.4	1.6	2049	9	AK027165	AK027165 Homo sapi
71	62.2	2.6	38000	8	AB004539	AB004539 Schizosac	c 144	39.4	1.6	34631	9	AP001115	AP001115 Homo sapi
72	58.8	2.5	125020	9	AF429315	AF429315 Homo sapi	c 145	39.4	1.6	39675	9	AP001117	AP001117 Homo sapi
73	58.6	2.4	5448	9	AK074064	AK074064 Homo sapi	c 146	39.4	1.6	153441	9	BS000071	BS000071 Pan trogl
74	53	2.2	578	6	AR412615	AR412615 Sequence	c 147	39.4	1.6	177622	2	AC023559	AC023559 Homo sapi
75	53	2.2	578	6	BD108168	BD108168 EST and e	c 148	39.4	1.6	180571	9	AC113425	AC113425 Homo sapi
76	52.4	2.2	1894	9	BC013987	BC013987 Homo sapi	c 149	39.4	1.6	340000	9	HS211C027	AL163227 Homo sapi
77	51	2.1	86765	9	AC004472	AC004472 Homo sapi	c 150	39.2	1.6	46996	9	AC112645	AC112645 Homo sapi
78	51	2.1	195102	9	AL353795	AL353795 Human DNA	c 151	39.2	1.6	99960	9	AC104637	AC104637 Homo sapi
79	51	2.1	198829	2	AL391668	AL391668 Homo sapi	c 152	39.2	1.6	187295	2	AC021531	AC021531 Homo sapi
80	49.2	2.0	125020	9	AF429315	AF429315 Sequence	c 153	39	1.6	2766	9	AK125744	AK125744 Homo sapi
81	48	2.0	125020	9	AF429315	AF429315 Homo sapi	c 154	39	1.6	132254	3	AC116330	AC116330 Dictyoste
82	46.2	1.9	2000	6	AX655393	AX655393 Sequence	c 155	39	1.6	160770	2	AC016796	AC016796 Homo sapi
83	45.6	1.9	3608	8	SCYLL031C	Z73136 S.cerevisia	c 156	39	1.6	170262	9	AC105398	AC105398 Homo sapi
84	44.8	1.9	786	11	CNS06K4V	AL402437 T3 end of	c 157	39	1.6	190651	9	AL353811	AL353811 Human DNA
85	44.4	1.9	1838	9	BC001030	BC001030 Homo sapi	c 158	38.8	1.6	832	6	AR415176	AR415176 Sequence
86	44.4	1.9	3048	6	AX488862	AX488862 Sequence	c 159	38.8	1.6	832	6	BD110729	BD110729 EST and e
87	43	1.8	124230	10	AC005259	AC005259 Mouse BAC	c 160	38.8	1.6	3492	6	AX226561	AX226561 Sequence
88	43	1.8	180424	9	AC106860	AC106860 Homo sapi	c 161	38.8	1.6	3493	6	AX226562	AX226562 Sequence
89	43	1.8	208030	10	AL672276	AL672276 Mouse DNA	c 162	38.8	1.6	9045	6	AX223857	AX223857 Sequence
90	42.2	1.8	186160	10	AC117213	AC117213 Mus muscu	c 163	38.8	1.6	9087	6	AX226507	AX226507 Sequence
91	42.2	1.8	231684	2	AC133955	AC133955 Mus muscu	c 164	38.8	1.6	11389	6	AX549158	AX549158 Sequence
92	42	1.8	7218	6	I66494	I66494 Sequence 14	c 165	38.8	1.6	11389	9	AF231024	AF231024 Homo sapi
93	41.8	1.7	142533	2	AC138160	AC138160 Rattus no	c 166	38.8	1.6	94516	8	AP004526	AP004526 Lotus cor
94	41.8	1.7	195988	2	AC141493	AC141493 Rattus no	c 167	38.8	1.6	111739	9	AF165424	AF165424 Homo sapi
95	41.8	1.7	276193	2	AC094506	AC094506 Rattus no	c 168	38.8	1.6	112655	9	AC103760	AC103760 Homo sapi
96	41.8	1.7	306781	2	AC119382	AC119382 Rattus no	c 169	38.8	1.6	120206	9	HS439F8	AL021392 Human DNA
97	41.6	1.7	235236	5	AL954130	AL954130 Zebrafish	c 170	38.8	1.6	132843	9	AC083845	AC083845 Homo sapi
98	41	1.7	146575	2	AC135571	AC135571 Rattus no	c 171	38.8	1.6	142477	2	BS321889	BS321889 Danio rer
99	41	1.7	152306	2	AC117759	AC117759 Mus muscu	c 172	38.8	1.6	163460	2	AC069378	AC069378 Homo sapi
100	41	1.7	153890	2	AC092525	AC092525 Papio anu	c 173	38.8	1.6	166039	2	AC044855	AC044855 Homo sapi
101	41	1.7	161194	2	AC021466	AC021466 Mus muscu	c 174	38.8	1.6	191786	2	AC137533	AC137533 Bos tauru
102	41	1.7	165110	2	AC121317	AC121317 Mus muscu	c 175	38.8	1.6	215911	10	AC126957	AC126957 Rattus no
103	41	1.7	215985	2	AC137029	AC137029 Rattus no	c 176	38.8	1.6	229806	2	AC146954	AC146954 Ootlemur
104	41	1.7	231268	2	AC118318	AC118318 Rattus no	c 177	38.8	1.6	250932	2	AC097598	AC097598 Rattus no
105	41	1.7	240453	2	AC103204	AC103204 Rattus no	c 178	38.8	1.6	308826	2	AC118525	AC118525 Rattus no
106	41	1.7	241998	2	AC112739	AC112739 Rattus no	c 179	38.8	1.6	347050	3	PFA929351	AL929351 Plasmodiu
107	41	1.7	249846	2	AC117758	AC117758 Mus muscu	c 180	38.6	1.6	93754	2	AC138754	AC138754 Homo sapi
108	40.8	1.7	134971	2	AC116367	AC116367 Oryza sat	c 181	38.6	1.6	162503	9	AL357772	AL357772 Human DNA
109	40.6	1.7	839	11	BV017453	BV017453 S212P6014	c 182	38.6	1.6	179173	10	AL669973	AL669973 Mouse DNA
110	40.4	1.7	76485	3	AC024211	AC024211 Caenorhab	c 183	38.6	1.6	213109	2	AC134199	AC134199 Rattus no
111	40.4	1.7	76485	3	AC024872	AC024872 Caenorhab	c 184	38.6	1.6	252459	2	AC094717	AC094717 Rattus no
112	40.4	1.7	108865	9	HS0345E4	AL132661 Human DNA	c 185	38.4	1.6	31043	1	AY268081	AY268081 Candidatu
113	40.4	1.7	115393	8	AC091247	AC091247 Oryza sat	c 186	38.4	1.6	109477	9	AC104042	AC104042 Homo sapi
114	40.4	1.7	117505	8	AC096687	AC096687 Oryza sat	c 187	38.4	1.6	110779	9	BX470173	BX470173 Human DNA
115	40.4	1.7	140661	2	AC012425	AC012425 Homo sapi	c 188	38.4	1.6	117780	8	AP003988	AP003988 Oryza sat
116	40.4	1.7	145268	2	AC119340	AC119340 Rattus no	c 189	38.4	1.6	164798	9	AC092598	AC092598 Homo sapi
117	40.2	1.7	43543	6	AX711964	AX711964 Sequence	c 190	38.4	1.6	190325	9	AL732327	AL732327 Human DNA
118	40.2	1.7	92179	9	AL390965	AL390965 Human DNA	c 191	38.4	1.6	289967	2	BS511031	BS511031 Danio rer
119	40.2	1.7	163595	2	AC022076	AC022076 Homo sapi	c 192	38.2	1.6	2473	9	BC027955	BC027955 Homo sapi
120	40.2	1.7	180465	9	AC074011	AC074011 Homo sapi	c 193	38.2	1.6	131144	10	AL645569	AL645569 Mouse DNA
121	40.2	1.7	222088	2	AC079216	AC079216 Mus muscu	c 194	38.2	1.6	160794	2	AC124751	AC124751 Mus muscu
122	40.2	1.7	260668	2	AC069469	AC069469 Mus muscu	c 195	38	1.6	60583	8	AX055482	AX055482 Sequence
123	40	1.7	5560	6	AX781118	AX781118 Sequence	c 196	38	1.6	134971	2	AC116367	AC116367 Arabidops
124	40	1.7	5561	6	AX780230	AX780230 Sequence	c 197	38	1.6	179163	2	AC117985	AC117985 Papio anu
125	40	1.7	5745	6	AX405586	AX405586 Sequence	c 198	38	1.6	180715	2	AC116932	AC116932 Papio anu
126	40	1.7	6237	9	AB011117	AB011117 Homo sapi	c 199	38	1.6	184582	9	AC010207	AC010207 Homo sapi
127	40	1.7	173119	9	AC079073	AC079073 Homo sapi	c 200	38	1.6	195138	2	AC118118	AC118118 Rattus no
128	40	1.7	174670	2	AC068281	AC068281 Homo sapi	c 201	38	1.6	235583	2	AC105659	AC105659 Rattus no
129	40	1.7	188972	2	AC006907	AC006907 Caenorhab	c 202	38	1.6	101981	9	AC003001	AC003001 Homo sapi
130	40	1.7	256744	2	AC132718	AC132718 Rattus no	c 203	37.8	1.6	110000	2	LMFLCHR12_06	Continuation (7 of
131	40	1.7	282895	2	AC096056	AC096056 Rattus no	c 204	37.8	1.6	112646	9	AC010240	AC010240 Homo sapi
132	39.8	1.7	120185	8	AC007138	AC007138 Arabidops	c 205	37.8	1.6	137132	9	AC136628	AC136628 Homo sapi
133	39.8	1.7	198220	8	ATCHRIV5	AL161493 Arabidops	c 206	37.8	1.6	153650	9	AC022296	AC022296 Homo sapi
134	39.8	1.7	198697	8	ATCHRIV4	AL161492 Arabidops	c 207	37.8	1.6	155304	9	AC055845	AC055845 Homo sapi
135	39.8	1.7	232443	2	AC099251	AC099251 Rattus no	c 208	37.8	1.6	157088	10	AC127292	AC127292 Mus muscu
136	39.8	1.7	266295	2	AC103500	AC103500 Rattus no	c 209	37.8	1.6	167446	2	AC137718	AC137718 Homo sapi
137	39.6	1.7	958	11	CNS06JEX	AL401503 T3 end of	c 210	37.8	1.6	177669	9	CNS05TE7	AL358336 Human chr
138	39.6	1.7	7218	6	I66494	I66494 Sequence 14	c 211	37.8	1.6				

C 212	37.8	1.6	179940	2	AC144813	AC144813 Mus muscu
213	37.8	1.6	180336	2	AC021731	AC021731 Homo sapi
C 214	37.8	1.6	180785	2	AC123979	AC123979 Papio anu
C 215	37.8	1.6	183902	9	AP003403	AP003403 Homo sapi
C 216	37.8	1.6	185953	2	AC136593	AC136593 Homo sapi
C 217	37.8	1.6	191603	2	AC110561	AC110561 Mus muscu
218	37.8	1.6	195843	2	AC023944	AC023944 Homo sapi
219	37.8	1.6	200675	2	AP004244	AP004244 Homo sapi
C 220	37.8	1.6	207298	2	AC136631	AC136631 Homo sapi
C 221	37.8	1.6	208472	10	AL833799	AL833799 Mouse DNA
C 222	37.8	1.6	220632	2	AC136596	AC136596 Homo sapi
223	37.6	1.6	37100	9	HS566H6	AL031845 Human DNA
224	37.6	1.6	98261	9	HS1054C24	AL035249 Human DNA
C 225	37.6	1.6	128683	2	AC135793	AC135793 Oryza sat
226	37.6	1.6	160545	9	AC036214	AC036214 Homo sapi
C 227	37.6	1.6	174347	10	AL928956	AL928956 Mouse DNA
C 228	37.6	1.6	180535	9	AC018952	AC018952 Homo sapi
C 229	37.6	1.6	196083	2	AC027092	AC027092 Homo sapi
C 230	37.4	1.6	446	6	AX676916	AX676916 Sequence
231	37.4	1.6	603	6	BD072152	BD072152 Secreted
232	37.4	1.6	2380	9	HSM808648	BM648500 Homo sapi
233	37.4	1.6	2403	9	BT006637	BT006637 Homo sapi
234	37.4	1.6	2421	9	HSARA1	Y14314 Homo sapien
235	37.4	1.6	2460	6	AX099535	AX099535 Sequence
236	37.4	1.6	2460	6	BD190805	BD190805 Secreted
237	37.4	1.6	2506	9	AB006198	AB006198 Homo sapi
238	37.4	1.6	2526	9	BC001058	BC001058 Homo sapi
239	37.4	1.6	2527	6	AR309144	AR309144 Sequence
240	37.4	1.6	2527	9	AF353625	AF353625 Homo sapi
241	37.4	1.6	2550	6	AX078301	AX078301 Sequence
C 242	37.4	1.6	5637	9	AK126983	AK126983 Homo sapi
C 243	37.4	1.6	37286	2	LMFL6852	AL034359 Leishmani
C 244	37.4	1.6	141819	5	AL935063	AL935063 Zebrafish
245	37.4	1.6	152468	2	AP001584	AP001584 Homo sapi
246	37.4	1.6	162328	9	AP000350	AP000350 Homo sapi
C 247	37.4	1.6	164840	2	AC011127	AC011127 Homo sapi
C 248	37.4	1.6	169553	9	AC022046	AC022046 Homo sapi
C 249	37.4	1.6	195782	9	AC074389	AC074389 Homo sapi
250	37.4	1.6	221926	2	BX005245	BX005245 Danio rer
C 251	37.4	1.6	247462	3	LMFLCHR4B	AL139794 Leishmani
C 252	37.4	1.6	252632	3	AB014818	AE014818 Plasmodiu
C 253	37.4	1.6	348077	1	AP003000	AP003000 Mesorhizo
C 254	37.2	1.6	4947	8	AF014927	AF014927 Chlamydom
255	37.2	1.6	9810	1	AF018073	AF018073 Rhodobact
256	37.2	1.6	9810	6	HD129571	HD129571 Polynucle
257	37.2	1.6	115499	2	AC130963	AC130963 Medicago
C 258	37.2	1.6	128590	2	AC009557	AC009557 Homo sapi
259	37.2	1.6	168448	9	AC009469	AC009469 Homo sapi
C 260	37.2	1.6	180189	5	BX005354	BX005354 Zebrafish
C 261	37.2	1.6	195848	10	AC117600	AC117600 Mus muscu
262	37	1.5	505	6	AR424142	AR424142 Sequence
263	37	1.5	505	6	BD119695	BD119695 EST and e
264	37	1.5	102477	9	AC008935	AC008935 Homo sapi
265	37	1.5	110000	2	AC120578_0	AC120578 Rattus no
266	37	1.5	110000	2	AC120578_1	Continuation (2 of
C 267	37	1.5	111990	9	AL360294	AL360294 Human DNA
C 268	37	1.5	123530	2	AL356369	AL356369 Homo sapi
C 269	37	1.5	161511	2	AC128773	AC128773 Rattus no
270	37	1.5	166357	9	AC091559	AC091559 Homo sapi
C 271	37	1.5	169862	2	AC025530	AC025530 Homo sapi
C 272	37	1.5	170358	9	AC008873	AC008873 Homo sapi
C 273	37	1.5	172138	2	AC064796	AC064796 Homo sapi
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275	37	1.5	182829	10	AL627214	AL627214 Mouse DNA
C 276	37	1.5	183246	2	AC118486	AC118486 Rattus no
277	37	1.5	183389	2	AC110168	AC110168 Mus muscu
C 278	37	1.5	184118	9	AC016580	AC016580 Homo sapi
279	37	1.5	188559	2	AC124602	AC124602 Mus muscu
C 280	37	1.5	194965	2	AC121018	AC121018 Rattus no
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284	37	1.5	221805	10	AC105515	AC105515 Rattus no
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286	37	1.5	236974	2	AC095207	AC095207 Rattus no
287	37	1.5	240833	2	AC107087	AC107087 Rattus no
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289	37	1.5	255459	2	AC127743	AC127743 Rattus no
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296	36.8	1.5	5399	10	RNGMTG	X07833 Rat glycine
297	36.8	1.5	85702	8	AC020665	AC020665 Arabidops
C 298	36.8	1.5	95169	8	AP006084	AP006084 Lotus cor
299	36.8	1.5	101739	9	AL591400	AL591400 Human DNA
C 300	36.8	1.5	124659	9	AL583828	AL583828 Human DNA
C 301	36.8	1.5	137312	2	AC141039	AC141039 Rattus no
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C 303	36.8	1.5	141186	2	AC015578	AC015578 Homo sapi
C 304	36.8	1.5	148452	2	AL954696	AL954696 Danio rer
305	36.8	1.5	153108	9	AL355273	AL355273 Human DNA
306	36.8	1.5	158745	9	AL136456	AL136456 Human DNA
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310	36.8	1.5	166207	9	AL135785	AL135785 Human DNA
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312	36.8	1.5	178193	2	AC068949	AC068949 Homo sapi
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315	36.8	1.5	185560	2	AC129046	AC129046 Rattus no
C 316	36.8	1.5	194290	2	AC137228	AC137228 Rattus no
317	36.8	1.5	194317	2	AC137232	AC137232 Rattus no
318	36.8	1.5	197626	10	AC115117	AC115117 Mus muscu
C 319	36.8	1.5	216747	2	AC120299	AC120299 Rattus no
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321	36.8	1.5	256944	2	AC096512	AC096512 Rattus no
322	36.8	1.5	267649	2	AC128452	AC128452 Rattus no
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324	36.6	1.5	364	6	AR425705	AR425705 Sequence
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C 336	36.6	1.5	94959	2	AC136765	AC136765 Homo sapi
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338	36.6	1.5	110257	8	AC144609	AC144609 Medicago
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C 342	36.6	1.5	129169	2	AC032038	AC032038 Homo sapi
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C 355	36.6	1.5	212199	9	AL445199	AL445199 Human DNA
356	36.6	1.5	213047	2	AC020557	AC020557 Homo sapi
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C 361	36.6	1.5	340000	9	AP001746	AP001746 Homo sapi	434	1.5	2039	9	AK126250	AK126250 Homo sapi
C 362	36.6	1.5	348178	1	BX572092	BX572092 Prochloro	435	1.5	4088	9	AK128869	AK128869 Homo sapi
C 363	36.4	1.5	714	6	AX763031	AX763031 Sequence	436	1.5	4494	9	AK024476	AK024476 Homo sapi
C 364	36.4	1.5	2942	1	RPUS5213	U55213 Rickettsia	437	1.5	25815	9	HS321D2	AL031033 Human DNA
C 365	36.4	1.5	3325	5	AF117612	AF117612 Gallus ga	438	1.5	37144	2	BX293534	BX293534 Danio rer
C 366	36.4	1.5	10502	1	AE014645	AE014645 Bifidobac	C 439	1.5	64674	9	AC087057	AC087057 Homo sapi
C 367	36.4	1.5	65748	9	AL445666	AL445666 Human DNA	C 440	1.5	71166	2	AC023783	AC023783 Homo sapi
C 368	36.4	1.5	103995	2	AC096695	AC096695 Rattus no	C 441	1.5	95579	9	AC023162	AC023162 Homo sapi
C 369	36.4	1.5	123379	2	AC119409	AC119409 Medicago	442	1.5	98356	9	HS344J2	AL449213 Homo sapi
C 370	36.4	1.5	123672	2	AC121246	AC121246 Medicago	443	1.5	110000	2	BX649565	Continuation (3 of
C 371	36.4	1.5	150021	5	BX088691	BX088691 Zebrafish	C 444	1.5	110000	3	AC116957	AC116957 Dictyoste
C 372	36.4	1.5	158716	2	AC102318	AC102318 Mus muscu	445	1.5	112058	2	AC055112	AC055112 Homo sapi
C 373	36.4	1.5	160434	2	AC018590	AC018590 Homo sapi	446	1.5	126083	9	AC105337	AC105337 Homo sapi
C 374	36.4	1.5	166748	2	AC115533	AC115533 Papio anu	C 447	1.5	135153	9	AL353605	AL353605 Human DNA
C 375	36.4	1.5	169283	2	AC044820	AC044820 Homo sapi	C 448	1.5	148008	2	AC092004	AC092004 Bos tauru
C 376	36.4	1.5	169510	2	AC130006	AC130006 Rattus no	C 449	1.5	149471	2	AP005921	AP005921 Oryza sat
C 377	36.4	1.5	184296	9	AC099047	AC099047 Homo sapi	C 450	1.5	154485	2	AC116894	AC116894 Mus muscu
C 378	36.4	1.5	187024	2	AC102093	AC102093 Mus muscu	C 451	1.5	154616	2	AC067772	AC067772 Homo sapi
C 379	36.4	1.5	212238	2	AC134077	AC134077 Rattus no	C 452	1.5	155770	2	AC092381	AC092381 Homo sapi
C 380	36.4	1.5	219457	2	AC095833	AC095833 Rattus no	453	1.5	159082	9	AC025947	AC025947 Homo sapi
C 381	36.4	1.5	220710	2	AC125304	AC125304 Rattus no	454	1.5	164396	2	HSAC000380	AC092008 Bos tauru
C 382	36.4	1.5	231986	2	AC097904	AC097904 Rattus no	C 455	1.5	170935	2	AC092008	AC092008 Bos tauru
C 383	36.4	1.5	234639	2	AC145118	AC145118 Rattus no	C 456	1.5	172332	2	AC117167	AC117167 Rattus no
C 384	36.4	1.5	237586	2	AC095836	AC095836 Rattus no	457	1.5	172777	9	AC026395	AC026395 Homo sapi
C 385	36.4	1.5	238242	2	AC102152	AC102152 Mus muscu	458	1.5	174298	2	AC120514	AC120514 Bos tauru
C 386	36.4	1.5	242084	2	AC130525	AC130525 Rattus no	459	1.5	174938	9	AC067801	AC067801 Homo sapi
C 387	36.4	1.5	245425	2	AC097338	AC097338 Rattus no	C 460	1.5	175970	9	AC097488	AC097488 Homo sapi
C 388	36.4	1.5	245462	2	AC107264	AC107264 Rattus no	C 461	1.5	179071	2	AC146665	AC146665 Homo sapi
C 389	36.4	1.5	253329	2	AC094801	AC094801 Rattus no	462	1.5	184987	5	BX572633	BX572633 Zebrafish
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C 393	36.4	1.5	302675	1	AP005024	AP005024 Streptomy	466	1.5	194851	9	AC079264	AC079264 Homo sapi
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C 398	36.2	1.5	7883	1	MEU87316	U87316 Methylobact	C 471	1.5	227942	9	AP002856	AP002856 Homo sapi
C 399	36.2	1.5	10444	1	AE007836	AE007836 Clostridi	C 472	1.5	234060	2	AC112402	AC112402 Rattus no
C 400	36.2	1.5	12606	1	AE005995	AE005995 Caulobact	473	1.5	243356	2	AC132061	AC132061 Rattus no
C 401	36.2	1.5	19897	3	AC006623	AC006623 Caenorhab	C 474	1.5	249325	2	AC073833	AC073833 Homo sapi
C 402	36.2	1.5	19897	3	AC024090	AC024090 Caenorhab	475	1.5	253946	2	AC105161	AC105161 Mus muscu
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C 406	36.2	1.5	77536	6	AR271638	AC084245 Homo sapi	35.8	1.5	2171	9	BC028918	BC028918 Homo sapi
C 407	36.2	1.5	99928	2	AC084245	AJ320506 Mus muscu	35.8	1.5	2677	9	AK026105	AK026105 Homo sapi
C 408	36.2	1.5	111805	10	MMU320506	AL513211 Human DNA	480	1.5	3257	9	AY026527	AY026527 Homo sapi
C 409	36.2	1.5	126228	9	AL513211	AL590035 Human DNA	481	1.5	3431	9	HSM802639	AL353935 Homo sapi
C 410	36.2	1.5	133397	9	AL590035	AL512600 Human DNA	482	1.5	3866	9	AK124772	AK124772 Homo sapi
C 411	36.2	1.5	150814	2	AC134411	AC134411 Mus muscu	C 483	1.5	42106	1	MSG81133CS	L09740 Xenopus lae
C 412	36.2	1.5	151699	8	AP003916	AP003916 Oryza sat	C 484	1.5	6788	5	XELNMUSMYO	L78811 Mycobacteri
C 413	36.2	1.5	162760	9	AC007969	AC007969 Homo sapi	C 485	1.5	81124	2	BX005337	BX005337 Danio rer
C 414	36.2	1.5	173210	5	AL928968	AL928968 Zebrafish	C 486	1.5	81124	2	BX005337	BX005337 Danio rer
C 415	36.2	1.5	174648	9	AL691497	AL691497 Human DNA	C 487	1.5	96798	9	AL356420	AL356420 Human DNA
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C 420	36.2	1.5	200747	2	AC107681	AC107681 Mus muscu	C 493	1.5	130445	9	AC116648	AC116648 Homo sapi
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C 423	36.2	1.5	221651	2	AC107356	AC107356 Rattus no	C 496	1.5	156249	2	BX276184	BX276184 Danio rer
C 424	36.2	1.5	247251	2	AC131478	AC131478 Rattus no	C 497	1.5	160095	9	AC087798	AC087798 Homo sapi
C 425	36.2	1.5	252757	2	AC094658	AC094658 Rattus no	C 498	1.5	162685	2	AC022943	AC022943 Homo sapi
C 426	36.2	1.5	261708	2	AC098350	AC098350 Rattus no	C 499	1.5	175668	2	AC027268	AC027268 Homo sapi
C 427	36.2	1.5	272137	2	AC095976	AC095976 Rattus no	500	1.5	176825	10	AC132437	AC132437 Mus muscu
C 428	36.2	1.5	297079	2	AC105882	AC105882 Rattus no						
C 429	36	1.5	1713	6	AX440496	AX440496 Sequence						
C 430	36	1.5	1830	6	AX164141	AX164141 Sequence						

ALIGNMENTS

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RESULT 1
AX055478 LOCUS AX055478 2395 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 108 from Patent WO0073452.
ACCESSION AX055478
VERSION AX055478.1 GI:12228736
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
Tumas,D., Watanabe,C.K. and Wood,W.I.
TITLE Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 0073452-A 108 07-DEC-2000;
Genentech, Inc. (US)
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SOURCE					
ORGANISM					

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL Patent: WO 0193983-A 117 13-DEC-2001;

Genentech Inc. (US)

FEATURES location/Qualifiers

source 1..2395

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ORIGIN

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Db |||||
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DEFINITION	Sequence 291 from Patent WO0200690.
ACCESSION	AX4911184
VERSION	AX4911184.1 GI:22323929
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1
REFERENCE	Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
AUTHORS	

Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 020690-A 291 03-JAN-2002;
Genentech, Inc. (US)
FEATURES
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Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nhgri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 93 Row: n Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction.

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Best Local Similarity 91.0%; Pred. No. 0;
Matches 2151; Conservative 0; Mismatches 12; Indels 201; Gaps 2;

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DEFINITION Sequence 1769 from Patent EP1347046.
ACCESSION AX834645
VERSION AX834645.1 GI:39920780
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,

Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuho,Y.
Full-length cDNA sequences
Patent: EP 1347046-A 1769 24-SEP-2003;
Research Association for Biotechnology (JP)
Location/Qualifiers (JP)
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ORIGIN

Query Match 71.8%; Score 1719.4; DB 6; Length 2630;
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ACCESSION AK097244
VERSION AK097244.1 GI:21756934
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S., Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 2630)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI); (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

OS Homo sapiens (human)

PN JP 2002017375-A/2726

PD 22-JAN-2002

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SHINICHI KOJIMA,

PI TETSUJI OTSUKI,HISASHI KOGA

PC

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VERSION AK074815.1 GI:22760509
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
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Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Ninomiya,K.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3197)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5' - & 3' - end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
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ORIGIN

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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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JP 2002017375-A/3174.
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1 (bases 1 to 3019)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 3174 22-JAN-2002;
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PN JP 2002017375-A/3174
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SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
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DEFINITION Homo sapiens cDNA FLJ90234 fis, clone NT2RM2000565.

ACCESSION AK074715

VERSION AK074715.1 GI:22760337

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

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AUTHORS Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and Ninomiya,K.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3019)

AUTHORS Isogai,T. and Otsuki,T.

TITLE Direct Submission

JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).

FEATURES
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ORIGIN

Query Match 52.9%; Score 1266.6; DB 9; Length 3019;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1325; Conservative 0; Mismatches 4; Indels 46; Gaps 1;

QY 230 CTGGAGCCAGTTCTAACTGGACCACGCTGCCACCACCTCTCTCAGTAAAGTTGTTATTG 289

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GenCore version 5.1.6
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(without alignments)
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20	2395	100.0	2395	14	US-10-053-107-7	Sequence 7, Appl
21	2395	100.0	2395	15	US-10-035-855-44	Sequence 44, Appl
22	2395	100.0	2395	15	US-10-063-616-139	Sequence 139, Appl
23	2395	100.0	2395	15	US-10-063-502-139	Sequence 139, Appl
24	2395	100.0	2395	15	US-10-227-884-117	Sequence 117, Appl
25	2395	100.0	2395	15	US-10-036-214-44	Sequence 44, Appl
26	2395	100.0	2395	15	US-10-035-719-44	Sequence 44, Appl
27	2395	100.0	2395	15	US-10-230-163-117	Sequence 117, Appl
28	2395	100.0	2395	15	US-10-036-160-44	Sequence 44, Appl
29	2395	100.0	2395	15	US-10-230-338-117	Sequence 117, Appl
30	2395	100.0	2395	15	US-10-218-631-117	Sequence 117, Appl
31	2395	100.0	2395	15	US-10-035-958-44	Sequence 44, Appl
32	2395	100.0	2395	15	US-10-036-150-44	Sequence 44, Appl
33	2395	100.0	2395	15	US-10-063-518-139	Sequence 139, Appl
34	2395	100.0	2395	15	US-10-230-414-117	Sequence 117, Appl
35	2395	100.0	2395	15	US-10-063-598-139	Sequence 139, Appl
36	2395	100.0	2395	15	US-10-227-693-139	Sequence 139, Appl
37	2395	100.0	2395	15	US-10-213-145-7	Sequence 7, Appl
38	2395	100.0	2395	15	US-10-063-567-139	Sequence 139, Appl
39	2395	100.0	2395	15	US-10-216-159A-117	Sequence 117, Appl
40	2395	100.0	2395	15	US-10-218-849-117	Sequence 117, Appl
41	2395	100.0	2395	15	US-10-227-873-117	Sequence 117, Appl
42	2395	100.0	2395	15	US-10-227-883-117	Sequence 117, Appl
43	2395	100.0	2395	15	US-10-219-076-117	Sequence 117, Appl
44	2395	100.0	2395	15	US-10-230-434-117	Sequence 117, Appl
45	2395	100.0	2395	15	US-10-063-599-139	Sequence 139, Appl
46	2395	100.0	2395	15	US-10-213-199-7	Sequence 7, Appl
47	2395	100.0	2395	15	US-10-063-595-139	Sequence 139, Appl
48	2395	100.0	2395	15	US-10-219-003-117	Sequence 117, Appl
49	2395	100.0	2395	15	US-10-219-075-117	Sequence 117, Appl
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51	2395	100.0	2395	15	US-10-219-466-117	Sequence 117, Appl
52	2395	100.0	2395	15	US-10-219-479-117	Sequence 117, Appl
53	2395	100.0	2395	15	US-10-219-481-117	Sequence 117, Appl
54	2395	100.0	2395	15	US-10-230-260-117	Sequence 117, Appl
55	2395	100.0	2395	15	US-10-232-231-117	Sequence 117, Appl
56	2395	100.0	2395	15	US-10-232-233-117	Sequence 117, Appl
57	2395	100.0	2395	15	US-10-036-063-44	Sequence 44, Appl
58	2395	100.0	2395	15	US-10-216-165-117	Sequence 117, Appl
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62	2395	100.0	2395	15	US-10-219-536-117	Sequence 117, Appl
63	2395	100.0	2395	15	US-10-233-205-117	Sequence 117, Appl
64	2395	100.0	2395	15	US-10-219-072-117	Sequence 117, Appl
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66	2395	100.0	2395	15	US-10-219-474-117	Sequence 117, Appl
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68	2395	100.0	2395	15	US-10-219-528-117	Sequence 117, Appl
69	2395	100.0	2395	15	US-10-227-880-117	Sequence 117, Appl
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73	2395	100.0	2395	15	US-10-232-223-117	Sequence 117, Appl
74	2395	100.0	2395	15	US-10-232-225-117	Sequence 117, Appl
75	2395	100.0	2395	15	US-10-232-227-117	Sequence 117, Appl
76	2395	100.0	2395	15	US-10-232-229-117	Sequence 117, Appl
77	2395	100.0	2395	15	US-10-232-234-117	Sequence 117, Appl
78	2395	100.0	2395	15	US-10-219-060-117	Sequence 117, Appl
79	2395	100.0	2395	15	US-10-223-085-291	Sequence 291, Appl
80	2395	100.0	2395	15	US-10-216-160-117	Sequence 117, Appl
81	2395	100.0	2395	15	US-10-216-162-117	Sequence 117, Appl
82	2395	100.0	2395	15	US-10-216-164-117	Sequence 117, Appl
83	2395	100.0	2395	15	US-10-216-167-117	Sequence 117, Appl
84	2395	100.0	2395	15	US-10-216-168-117	Sequence 117, Appl
85	2395	100.0	2395	15	US-10-219-065-117	Sequence 117, Appl
86	2395	100.0	2395	15	US-10-219-071-117	Sequence 117, Appl
87	2395	100.0	2395	15	US-10-219-074-117	Sequence 117, Appl

234	2395	100.0	2395	15	US-10-063-684-139	Sequence 139, App	307	101.8	4.3	3671	13	US-10-194-463-265	Sequence 265, App
235	2395	100.0	2395	15	US-10-063-688-139	Sequence 139, App	308	101.8	4.3	3671	13	US-10-194-484-265	Sequence 265, App
236	2395	100.0	2395	15	US-10-223-081-291	Sequence 291, App	309	101.8	4.3	3671	13	US-10-195-884-265	Sequence 265, App
237	2395	100.0	2395	15	US-10-063-520-139	Sequence 139, App	310	101.8	4.3	3671	13	US-10-195-896-265	Sequence 265, App
238	2395	100.0	2395	15	US-10-063-647-139	Sequence 139, App	311	101.8	4.3	3671	13	US-10-196-744-265	Sequence 265, App
239	2395	100.0	2395	15	US-10-218-765-117	Sequence 117, App	312	101.8	4.3	3671	13	US-10-196-755-265	Sequence 265, App
240	2395	100.0	2395	15	US-10-219-063-117	Sequence 117, App	313	101.8	4.3	3671	13	US-10-196-757-265	Sequence 265, App
241	2395	100.0	2395	15	US-10-219-066-117	Sequence 117, App	314	101.8	4.3	3671	13	US-10-197-704-265	Sequence 265, App
242	2395	100.0	2395	15	US-10-219-067-117	Sequence 117, App	315	101.8	4.3	3671	13	US-10-197-710-265	Sequence 265, App
243	2395	100.0	2395	15	US-10-219-068-117	Sequence 117, App	316	101.8	4.3	3671	13	US-10-198-758-265	Sequence 265, App
244	2395	100.0	2395	15	US-10-219-069-117	Sequence 117, App	317	101.8	4.3	3671	13	US-10-198-766-265	Sequence 265, App
245	2395	100.0	2395	15	US-10-219-073-117	Sequence 117, App	318	101.8	4.3	3671	13	US-10-199-304-265	Sequence 265, App
246	2395	100.0	2395	15	US-10-219-475-117	Sequence 117, App	319	101.8	4.3	3671	13	US-10-199-309-265	Sequence 265, App
247	2395	100.0	2395	15	US-10-219-480-117	Sequence 117, App	320	101.8	4.3	3671	13	US-10-199-313-265	Sequence 265, App
248	2395	100.0	2395	15	US-10-219-483-117	Sequence 117, App	321	101.8	4.3	3671	13	US-10-199-456-265	Sequence 265, App
249	2395	100.0	2395	15	US-10-219-525-117	Sequence 117, App	322	101.8	4.3	3671	13	US-10-201-329-265	Sequence 265, App
250	2395	100.0	2395	15	US-10-219-526-117	Sequence 117, App	323	101.8	4.3	3671	13	US-10-202-412-265	Sequence 265, App
251	2395	100.0	2395	15	US-10-219-530-117	Sequence 117, App	324	101.8	4.3	3671	13	US-10-206-919-265	Sequence 265, App
252	2395	100.0	2395	15	US-10-219-531-117	Sequence 117, App	325	101.8	4.3	3671	13	US-10-206-922-265	Sequence 265, App
253	2395	100.0	2395	15	US-10-219-532-117	Sequence 117, App	326	101.8	4.3	3671	13	US-10-206-924-265	Sequence 265, App
254	2395	100.0	2395	15	US-10-219-533-117	Sequence 117, App	327	101.8	4.3	3671	13	US-10-206-928-265	Sequence 265, App
255	2395	100.0	2395	15	US-10-230-437-117	Sequence 117, App	328	101.8	4.3	3671	13	US-10-207-914-265	Sequence 265, App
256	2395	100.0	2395	15	US-10-232-228-117	Sequence 117, App	329	101.8	4.3	3671	13	US-10-207-921-265	Sequence 265, App
257	2395	100.0	2395	15	US-10-063-548-139	Sequence 139, App	330	101.8	4.3	3671	13	US-10-207-922-265	Sequence 265, App
258	2395	100.0	2395	15	US-10-063-578-139	Sequence 139, App	331	101.8	4.3	3671	13	US-10-208-027-265	Sequence 265, App
259	2395	100.0	2395	15	US-10-063-648-139	Sequence 139, App	332	101.8	4.3	3671	13	US-10-174-570-265	Sequence 265, App
260	2395	100.0	2395	15	US-10-063-677-139	Sequence 139, App	333	101.8	4.3	3671	13	US-10-183-005-265	Sequence 265, App
261	2395	100.0	2395	15	US-10-063-718-139	Sequence 139, App	334	101.8	4.3	3671	13	US-10-226-254A-101	Sequence 101, App
262	2395	100.0	2395	15	US-10-063-741-139	Sequence 139, App	335	101.8	4.3	3671	14	US-10-052-586-265	Sequence 265, App
263	2395	100.0	2395	15	US-10-063-617-139	Sequence 139, App	336	101.8	4.3	3671	15	US-10-174-590-265	Sequence 265, App
264	2395	100.0	2395	15	US-10-223-082-291	Sequence 291, App	337	101.8	4.3	3671	15	US-10-176-758-265	Sequence 265, App
265	2395	100.0	2395	15	US-10-063-664-139	Sequence 139, App	338	101.8	4.3	3671	15	US-10-175-737-265	Sequence 265, App
266	2395	100.0	2395	15	US-10-063-561-139	Sequence 139, App	339	101.8	4.3	3671	15	US-10-173-706-265	Sequence 265, App
267	2395	100.0	2395	15	US-10-063-618-139	Sequence 139, App	340	101.8	4.3	3671	15	US-10-175-738-265	Sequence 265, App
268	2395	100.0	2395	15	US-10-063-657-139	Sequence 139, App	341	101.8	4.3	3671	15	US-10-175-752-265	Sequence 265, App
269	2395	100.0	2395	15	US-10-063-668-139	Sequence 139, App	342	101.8	4.3	3671	15	US-10-176-482-265	Sequence 265, App
270	2395	100.0	2395	16	US-10-063-550-139	Sequence 139, App	343	101.8	4.3	3671	15	US-10-176-757-265	Sequence 265, App
271	2395	100.0	2395	16	US-10-232-226-117	Sequence 117, App	344	101.8	4.3	3671	15	US-10-176-913-265	Sequence 265, App
272	2395	100.0	2395	16	US-10-230-130-117	Sequence 117, App	345	101.8	4.3	3671	15	US-10-180-552-265	Sequence 265, App
273	2395	100.0	2395	17	US-10-119-480-117	Sequence 117, App	346	101.8	4.3	3671	15	US-10-180-557-265	Sequence 265, App
274	1719.4	71.8	2630	16	US-10-108-260A-1769	Sequence 1769, App	347	101.8	4.3	3671	15	US-10-173-700-265	Sequence 265, App
275	1520.4	63.5	1725	13	US-10-063-512-139	Sequence 139, App	348	101.8	4.3	3671	15	US-10-174-572-265	Sequence 265, App
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277	455.6	19.0	500	10	US-09-918-995-21372	Sequence 21372, App	350	101.8	4.3	3671	15	US-10-174-582-265	Sequence 265, App
278	324.4	13.5	2039	13	US-10-342-887-1701	Sequence 1701, App	351	101.8	4.3	3671	15	US-10-174-588-265	Sequence 265, App
279	324.4	13.5	2039	13	US-10-172-118-1701	Sequence 1701, App	352	101.8	4.3	3671	15	US-10-175-739-265	Sequence 265, App
280	134	5.6	480	10	US-09-814-353-13689	Sequence 13689, App	353	101.8	4.3	3671	15	US-10-175-740-265	Sequence 265, App
281	131	5.5	411	10	US-09-814-353-933	Sequence 933, App	354	101.8	4.3	3671	15	US-10-175-743-265	Sequence 265, App
282	131	5.5	411	10	US-09-814-353-7304	Sequence 7304, App	355	101.8	4.3	3671	15	US-10-176-488-265	Sequence 265, App
283	101.8	4.3	3671	10	US-09-946-374-101	Sequence 101, App	356	101.8	4.3	3671	15	US-10-176-492-265	Sequence 265, App
284	101.8	4.3	3671	12	US-10-015-395A-101	Sequence 101, App	357	101.8	4.3	3671	15	US-10-176-747-265	Sequence 265, App
285	101.8	4.3	3671	13	US-10-206-915-265	Sequence 265, App	358	101.8	4.3	3671	15	US-10-176-750-265	Sequence 265, App
286	101.8	4.3	3671	13	US-10-199-670-265	Sequence 265, App	359	101.8	4.3	3671	15	US-10-176-985-265	Sequence 265, App
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289	101.8	4.3	3671	13	US-10-208-024-265	Sequence 265, App	362	101.8	4.3	3671	15	US-10-176-993-265	Sequence 265, App
290	101.8	4.3	3671	13	US-10-201-853-265	Sequence 265, App	363	101.8	4.3	3671	15	US-10-184-658-265	Sequence 265, App
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296	101.8	4.3	3671	13	US-10-006-485A-101	Sequence 101, App	369	101.8	4.3	3671	15	US-10-174-585-265	Sequence 265, App
297	101.8	4.3	3671	13	US-10-013-907A-101	Sequence 101, App	370	101.8	4.3	3671	15	US-10-174-586-265	Sequence 265, App
298	101.8	4.3	3671	13	US-10-015-499A-101	Sequence 101, App	371	101.8	4.3	3671	15	US-10-175-747-265	Sequence 265, App
299	101.8	4.3	3671	13	US-10-176-484-265	Sequence 265, App	372	101.8	4.3	3671	15	US-10-176-481-265	Sequence 265, App
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302	101.8	4.3	3671	13	US-10-187-738-265	Sequence 265, App	375	101.8	4.3	3671	15	US-10-176-756-265	Sequence 265, App
303	101.8	4.3	3671	13	US-10-187-740-265	Sequence 265, App	376	101.8	4.3	3671	15	US-10-176-911-265	Sequence 265, App
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305	101.8	4.3	3671	13	US-10-194-363-265	Sequence 265, App	378	101.8	4.3	3671	15	US-10-176-925-265	Sequence 265, App
306	101.8	4.3	3671	13	US-10-194-460-265	Sequence 265, App	379	101.8	4.3	3671	15	US-10-176-925-265	Sequence 265, App

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428	101.8	4.3	3671	15	US-10-187-588-265	Sequence 265, App
429	101.8	4.3	3671	15	US-10-187-597-265	Sequence 265, App
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ALIGNMENTS

RESULT 1

US-09-931-836-44
; Sequence 44, Application US/09931836
; Publication No. US20030027249A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C1
; CURRENT APPLICATION NUMBER: US/09/931,836
; CURRENT FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
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; PRIOR APPLICATION NUMBER: 60/113300
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; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 44
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-931-836-44

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-081-056-291
; Sequence 291, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P.Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C1
CURRENT APPLICATION NUMBER: US/10/081,056
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/219,556
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PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
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PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
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PRIOR APPLICATION NUMBER: US 09/643,657
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PRIOR APPLICATION NUMBER: PCT/US00/23328
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PRIOR APPLICATION NUMBER: US 09/866,028

PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/866,034
PRIOR FILING DATE: 2001-05-25
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PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/870,574
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17443
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/00000
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 291
LENGTH: 2395
TYPE: DNA
ORGANISM: Homosapiens
US-10-081-056-291
Query Match 100.0%; Score 2395; DB 13; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCGGCATC 60
Db 1 CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCGGCATC 60
QY 61 CAGCCTAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTTCGTTACCTGTTCGCTAGCG 120
Db 61 CAGCCTAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTTCGTTACCTGTTCGCTAGCG 120
QY 121 ATCGAGGTGCTAGGGATCGCGGTCTTCCCTTCGGGGATTTCCCGGTCCTCCGTTCTCC 180
Db 121 ATCGAGGTGCTAGGGATCGCGGTCTTCCCTTCGGGGATTTCCCGGTCCTCCGTTCTCC 180
QY 181 TCTGCCAGAGCGGAACACGAGCGGAGCCCGAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
Db 181 TCTGCCAGAGCGGAACACGAGCGGAGCCCGAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
QY 241 TCTAACTGGACACCGCTGCCACCCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGAT 300
Db 241 TCTAACTGGACACCGCTGCCACCCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGAT 300
QY 301 GCCTTGAGAGATGATTTTGTGTTTGGTCAAGGGGTGTGAAATTTATGCCCTACACAACT 360
Db 301 GCCTTGAGAGATGATTTTGTGTTTGGTCAAGGGGTGTGAAATTTATGCCCTACACAACT 360
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Db 361 TACCTTGTGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT 420
QY 421 ACTATGCTCGAATCAAGGCATTGATGACGGGGAGCCCTTCCCTGGCTTGTTCGACGTCTC 480
Db 421 ACTATGCTCGAATCAAGGCATTGATGACGGGGAGCCCTTCCCTGGCTTGTTCGACGTCTC 480
QY 481 AGGAACCTCAATTCTCTGCACCTGCTGGAAGACAGTGTGATAAGCAAGCAAAAGCAGCT 540
Db 481 AGGAACCTCAATTCTCTGCACCTGCTGGAAGACAGTGTGATAAGCAAGCAAAAGCAGCT 540
QY 541 GGAAGAAAGATAGTCTTTTATGGAGATGAAACCTGGGTTAAATTTATCCCAAGCATTTT 600
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Db 601 GTGGAATATGATGGAACAACCTCATTTTTCGTGTAGATTACAGAGGTGGATAATAAT 660
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; PRIOR FILING DATE: 1997-12-17									
; PRIOR APPLICATION NUMBER: 60/078910									
; PRIOR FILING DATE: 1998-03-20									
; PRIOR APPLICATION NUMBER: 60/079294									
; PRIOR FILING DATE: 1998-03-25									
; PRIOR APPLICATION NUMBER: 60/079656									
; PRIOR FILING DATE: 1998-03-26									
; PRIOR APPLICATION NUMBER: 60/079728									
; PRIOR FILING DATE: 1998-03-27									
; Remaining Prior Application data removed - See File Wrapper or PALM.									
; NUMBER OF SEQ ID NOS: 246									
; SEQ ID NO 117									
; LENGTH: 2395									
; TYPE: DNA									
; ORGANISM: Homo Sapien									
US-10-219-535-117									
Query Match 100.0%; Score 2395; DB 13; Length 2395;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	CCTGGAGCCGGAAGCGCGGTGCAGCAGGCGGAGGCTCCAGGTGGGGTCGGTTCGCGCATC	60						
Db	1	CCTGGAGCCGGAAGCGCGGTGCAGCAGGCGGAGGCTCCAGGTGGGGTCGGTTCGCGCATC	60						
QY	61	CAGCCTAGCGTGTCCACGATCGCGGTGGGCTCCGGGACTTTCGTAACCTGTTGCGTAGCG	120						
Db	61	CAGCCTAGCGTGTCCACGATCGCGGTGGGCTCCGGGACTTTCGTAACCTGTTGCGTAGCG	120						
QY	121	ATCGAGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATCTTCCGGCTCCCGTTCGTTCC	180						
Db	121	ATCGAGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATCTTCCGGCTCCCGTTCGTTCC	180						
QY	181	TCTGCCAGAGCGGAACACGGAGCGGAGCCCCAGCGCCGAAACCTTCGGCTGGAGCCAGT	240						
Db	181	TCTGCCAGAGCGGAACACGGAGCGGAGCCCCAGCGCCGAAACCTTCGGCTGGAGCCAGT	240						
QY	241	TCTAACTGGACCAACGCTGCCACCACTCTCTTCAGTAAAGTTGTTATTTCTGATAGAT	300						
Db	241	TCTAACTGGACCAACGCTGCCACCACTCTCTTCAGTAAAGTTGTTATTTCTGATAGAT	300						
QY	301	GCCTTGAGAGATGATTTGTGTTGGGTCAAAGGTGTGAAATTTATGCCCTACACAACT	360						
Db	301	GCCTTGAGAGATGATTTGTGTTGGGTCAAAGGTGTGAAATTTATGCCCTACACAACT	360						
QY	361	TACCTTGTGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAGCCACCTACAGTT	420						
Db	361	TACCTTGTGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAGCCACCTACAGTT	420						
QY	421	ACTATGCCTCGAATCAAGGCATTGATGACGGGGAGCCCTTCCTGGCTTGTGACGTCATC	480						
Db	421	ACTATGCCTCGAATCAAGGCATTGATGACGGGGAGCCCTTCCTGGCTTGTGACGTCATC	480						
QY	481	AGGAACCTCAATTCTCCTGCACTGTGTAAGACAGTGTGATAAGACAAGCAAGCAAGCAGCT	540						
Db	481	AGGAACCTCAATTCTCCTGCACTGTGTAAGACAGTGTGATAAGACAAGCAAGCAAGCAGCT	540						
QY	541	GGAAAAAGATAGTCTTTTATGGAGATGAAACCTGGGTAAATTTATCCCAAAGCATTTT	600						
Db	541	GGAAAAAGATAGTCTTTTATGGAGATGAAACCTGGGTAAATTTATCCCAAAGCATTTT	600						
QY	601	GTGGAATATGATGGAAACAACCTCAATTTTCGTGTCAGATTACACAGAGGTGGATAATAAT	660						
Db	601	GTGGAATATGATGGAAACAACCTCAATTTTCGTGTCAGATTACACAGAGGTGGATAATAAT	660						
QY	661	GTCACGAGGCATTTGGATAAAGTATTTAAAGAGGAGATTGGGACATATTAATCCTCCAC	720						
Db	661	GTCACGAGGCATTTGGATAAAGTATTTAAAGAGGAGATTGGGACATATTAATCCTCCAC	720						
QY	721	TACCTGGGGCTGACCAACATTGGCCACATTTAGGGCCCCAACAGCCCTGATTGGGCAG	780						
Db	721	TACCTGGGGCTGACCAACATTGGCCACATTTAGGGCCCCAACAGCCCTGATTGGGCAG	780						

QY	781	AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAG	840
Db	781	AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAG	840
QY	841	AGAGAGACGCCCTTTACCCAAATTTGCTGGTCTTTTGTGGTGACCATGGCATGTCTGAAACA	900
Db	841	AGAGAGACGCCCTTTACCCAAATTTGCTGGTCTTTTGTGGTGACCATGGCATGTCTGAAACA	900
QY	901	GGAAGTCACGGGGCCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT	960
Db	901	GGAAGTCACGGGGCCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT	960
QY	961	GCGTTTGAAAGGAAACCCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTG	1020
Db	961	GCGTTTGAAAGGAAACCCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTG	1020
QY	1021	GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTAGGAGCCTC	1080
Db	1021	GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTAGGAGCCTC	1080
QY	1081	CTATTCCCAGTTGTGGAAGAAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT	1140
Db	1081	CTATTCCCAGTTGTGGAAGAAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT	1140
QY	1141	ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAAATGTGCCGTATATGAAAAAGATCCTGGG	1200
Db	1141	ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAAATGTGCCGTATATGAAAAAGATCCTGGG	1200
QY	1201	TTTGAGCAGTTTAAATGTGAGAAAGATTGCAATGGGAACTGGATCAGACTGTACTGGAG	1260
Db	1201	TTTGAGCAGTTTAAATGTGAGAAAGATTGCAATGGGAACTGGATCAGACTGTACTGGAG	1260
QY	1261	GAAAAGCATTCAGAAAGTCTATTCAAACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT	1320
Db	1261	GAAAAGCATTCAGAAAGTCTATTCAAACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT	1320
QY	1321	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCAGTTCTCACCCGTCTCC	1380
Db	1321	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCAGTTCTCACCCGTCTCC	1380
QY	1381	TGCTCAGCGTCCACAGGCACCTGCACAGAAAGCTGAGCTGGAAGTCCCACGTCACTCTC	1440
Db	1381	TGCTCAGCGTCCACAGGCACCTGCACAGAAAGGCTGAGCTGGAAGTCCCACGTCACTCTC	1440
QY	1441	CTGGGTTTCTCTGCTCTTTTATTTTGGTGATCCTGGTCTTTTCGGCCGTTACAGTCATTG	1500
Db	1441	CTGGGTTTCTCTGCTCTTTTATTTTGGTGATCCTGGTCTTTTCGGCCGTTACAGTCATTG	1500
QY	1501	TGTGCACCTCAGCTGAAAAGTTCGTGCTACTTCTGTGGCCCTCTCGTGGCTGGCGCAGGCT	1560
Db	1501	TGTGCACCTCAGCTGAAAAGTTCGTGCTACTTCTGTGGCCCTCTCGTGGCTGGCGCAGGCT	1560
QY	1561	GCCTTTTCGTTTACAGACTCTGGTTGAAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCC	1620
Db	1561	GCCTTTTCGTTTACAGACTCTGGTTGAAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCC	1620
QY	1621	TGGACAGGGGCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCC	1680
Db	1621	TGGACAGGGGCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCC	1680
QY	1681	GACACAGGTGTTACATCTGTGCTGTGAGGTGAGTGCCTCAGTTCTTGGAAAGCTAGGT	1740
Db	1681	GACACAGGTGTTACATCTGTGCTGTGAGGTGAGTGCCTCAGTTCTTGGAAAGCTAGGT	1740
QY	1741	TCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACACAGGAACAAGCCCC	1800
Db	1741	TCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACACAGGAACAAGCCCC	1800
QY	1801	CAGCTGAGGGGTGTGTGAATCGGACAGCCTCCACAGCAGAGGTGTGGAGCTGCAGCTGA	1860
Db	1801	CAGCTGAGGGGTGTGTGAATCGGACAGCCTCCACAGCAGAGGTGTGGAGCTGCAGCTGA	1860
QY	1861	GGGAAGAAAGAGACAATCGGCCCTGGACACTCAGGAGGGTCAAAAAGGAGACTTGGTCGCACC	1920

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RESULT 6

US-10-063-513-139
; Sequence 139, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 139
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-513-139

Query Match 100.0%; Score 2395; DB 13; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGAGCCGGAAGCGCGGTGCAGCAGGCGGAGGCTCCAGGTGGGTCGGTTCGCGCATC 60
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Db 1441 CTGGGTTTCTCTGCTCTTTTATTGGTGATCCTGGTTCTTTTCGGCCGTTTACAGTCAATTG 1500
QY 1501 TGTGCACCTCAGCTGAAAAGTTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGAGGCT 1560
Db 1501 TGTGCACCTCAGCTGAAAAGTTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGAGGCT 1560
QY 1561 GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTCTGGCAGTGCCCC 1620
Db 1561 GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTCTGGCAGTGCCCC 1620
QY 1621 TGGACAGGGGGCCTCAGGGAAGGACGTTGAGCAGCCTTATCCAGGCCCTCTGGGTGTCCC 1680
Db 1621 TGGACAGGGGGCCTCAGGGAAGGACGTTGAGCAGCCTTATCCAGGCCCTCTGGGTGTCCC 1680


```
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,555
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 139
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-063-555-139

Query Match      100.0%; Score 2395; DB 13; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCTGGAGCCGGAAGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGTCCGATC 60
      |||
Db      1 CCTGGAGCCGGAAGCGGCTGCAGCAGGGCGAGGCTCCAGTGGGTCCGATC 60

QY      61 CAGCCTAGCGTGTCCACGATCGGCTGGGCTCCGGACTTTCGCTACCTGTTGCGTAGCG 120
      |||
Db      61 CAGCCTAGCGTGTCCACGATCGGCTGGGCTCCGGACTTTCGCTACCTGTTGCGTAGCG 120

QY      121 ATCGAGGTGCTAGGGATCGCGTCTTCCTTCGGGGATTCCTCCCGGCTCCCGTTCGTTCC 180
      |||
Db      121 ATCGAGGTGCTAGGGATCGCGTCTTCCTTCGGGGATTCCTCCCGGCTCCCGTTCGTTCC 180

QY      181 TCTGCCAGAGCGGAACACGAGGCGAGCCCCCAGCGCCCGAACCCCTCGCTGGAGCCAGT 240
      |||
Db      181 TCTGCCAGAGCGGAACACGAGGCGAGCCCCCAGCGCCCGAACCCCTCGCTGGAGCCAGT 240

QY      241 TCTAACTGGACCAAGCTGCTCCACCACTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGAT 300
      |||
Db      241 TCTAACTGGACCAAGCTGCTCCACCACTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGAT 300

QY      301 GCCTTGAGAGATGATTTTGTTGGGTCAAAGGTGTGAATTTATGCCCTACACAACT 360
      |||
Db      301 GCCTTGAGAGATGATTTTGTTGGGTCAAAGGTGTGAATTTATGCCCTACACAACT 360

QY      361 TACCTTGAGAGATGATTTTGTTGGGTCAAAGGTGTGAATTTATGCCCTACACAACT 420
      |||
Db      361 TACCTTGAGAGATGATTTTGTTGGGTCAAAGGTGTGAATTTATGCCCTACACAACT 420

QY      421 ACTATGCCTCGAATCAAGGCATTGATGACGGGAGCCCTTCCTGGCTTTGTCGACGTCATC 480
      |||
Db      421 ACTATGCCTCGAATCAAGGCATTGATGACGGGAGCCCTTCCTGGCTTTGTCGACGTCATC 480

QY      481 AGGAACCTCAATTCTCCTGCACCTGCTGGAAGACAGTGTGATAAGACAAGCAAGCAAGCT 540
      |||
Db      481 AGGAACCTCAATTCTCCTGCACCTGCTGGAAGACAGTGTGATAAGACAAGCAAGCAAGCT 540

QY      541 GGAAGAAAGATAGTCTTTTATGGAGATGAAACCTGGGTTAAATTATTTCCAAAGCATTTT 600
      |||
Db      541 GGAAGAAAGATAGTCTTTTATGGAGATGAAACCTGGGTTAAATTATTTCCAAAGCATTTT 600

QY      601 GTGGAATATGATGGAACAACCTCATTTTTCGTGTGATTAACAGAGGTGGATAATAAT 660
      |||
Db      601 GTGGAATATGATGGAACAACCTCATTTTTCGTGTGATTAACAGAGGTGGATAATAAT 660

QY      661 GTCAGGAGGCATTTGGATAAAGTATFAAAGAGGAGATTGAGACATATTAATCCTCCAC 720
      |||
Db      661 GTCAGGAGGCATTTGGATAAAGTATFAAAGAGGAGATTGAGACATATTAATCCTCCAC 720
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Db      661 GTCACGAGGCATTTGGATAAAGTATTAATAAGAGAGGAGATTGGGACATATTAATCCTCCAC 720

QY      721 TACCTGGGGCTGGACCAATTTGGCCACATTTTACGGGCCCAACAGCCCCCTGATTGGGAG 780
      |||
Db      721 TACCTGGGGCTGGACCAATTTGGCCACATTTTACGGGCCCAACAGCCCCCTGATTGGGAG 780

QY      781 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAG 840
      |||
Db      781 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAG 840

QY      841 AGAGAGACGCCCTTTACCCCAATTTGCTGGTCTTTTGTGGTGACCATGGCATGTCTGAAACA 900
      |||
Db      841 AGAGAGACGCCCTTTACCCCAATTTGCTGGTCTTTTGTGGTGACCATGGCATGTCTGAAACA 900

QY      901 GGAAGTCACGGGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT 960
      |||
Db      901 GGAAGTCACGGGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT 960

QY      961 GCGTTTGAAGAGAAACCCGGTGATATCCGACATCCAAAGCAGTCCAAATAGACGGATGTG 1020
      |||
Db      961 GCGTTTGAAGAGAAACCCGGTGATATCCGACATCCAAAGCAGTCCAAATAGACGGATGTG 1020

QY      1021 GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTC 1080
      |||
Db      1021 GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTC 1080

QY      1081 CTATTCCCAGTTGTGGAAAGGAACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
      |||
Db      1081 CTATTCCCAGTTGTGGAAAGGAACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140

QY      1141 ACAGTGCAGCTTAGTAAACTGTGCAAGAGAATGTGCCGTGCATATGAAAAGATCCTGGG 1200
      |||
Db      1141 ACAGTGCAGCTTAGTAAACTGTGCAAGAGAATGTGCCGTGCATATGAAAAGATCCTGGG 1200

QY      1201 TTTGAGCAGTTTAAATGTGAGAAAGATTGCAATGGGAACAGTGTGATCTTGGAG 1260
      |||
Db      1201 TTTGAGCAGTTTAAATGTGAGAAAGATTGCAATGGGAACAGTGTGATCTTGGAG 1260

QY      1261 GAAAAGCATTGAGAAAGTCTTAACTCAACCTGGGCTCCAAGTTCTCAGGAGTACCTGGAT 1320
      |||
Db      1261 GAAAAGCATTGAGAAAGTCTTAACTCAACCTGGGCTCCAAGTTCTCAGGAGTACCTGGAT 1320

QY      1321 GCTCTGAAGACGCTGAGCTTGTTCCTGAGTGCAACAGTGGGCCAGTTCTCACCCCTGCTCC 1380
      |||
Db      1321 GCTCTGAAGACGCTGAGCTTGTTCCTGAGTGCAACAGTGGGCCAGTTCTCACCCCTGCTCC 1380

QY      1381 TGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACCTGTCTATCTC 1440
      |||
Db      1381 TGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACCTGTCTATCTC 1440

QY      1441 CTGGGTTTCTCTGCTCTTTTATTTTGGTGATCCTGGTCTTTTCGGCCGTTTCAAGTCTATG 1500
      |||
Db      1441 CTGGGTTTCTCTGCTCTTTTATTTGGTGATCCTGGTCTTTTCGGCCGTTTCAAGTCTATG 1500

QY      1501 TGTGCACCTCAGCTGAAAGTTGCTGCTACTTCTGTGGCCCTCTCGTGGCTGGCGGAGGCT 1560
      |||
Db      1501 TGTGCACCTCAGCTGAAAGTTGCTGCTACTTCTGTGGCCCTCTCGTGGCTGGCGGAGGCT 1560

QY      1561 GCCTTTGTTTACCAGACTCTGGTTGAACACCTGGTGTGTCCTCAAGTGTGGCAGTGCCTC 1620
      |||
Db      1561 GCCTTTGTTTACCAGACTCTGGTTGAACACCTGGTGTGTCCTCAAGTGTGGCAGTGCCTC 1620

QY      1621 TGGACAGGGGGCCTCAGGGAAGGACGTTGGAGCAGCCTTATCCAGGCCCTCTGGGTGTCCTC 1680
      |||
Db      1621 TGGACAGGGGGCCTCAGGGAAGGACGTTGGAGCAGCCTTATCCAGGCCCTCTGGGTGTCCTC 1680

QY      1681 GACACAGGTGTTACATCTGTGCTGTGAGGTGAGTGCCTCAGTTCTTGGAAAGCTAGGT 1740
      |||
Db      1681 GACACAGGTGTTACATCTGTGCTGTGAGGTGAGTGCCTCAGTTCTTGGAAAGCTAGGT 1740

QY      1741 TCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCC 1800
      |||
Db      1741 TCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCC 1800
```



```
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,553
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 139
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-553-139

Query Match      100.0%; Score 2395; DB 13; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCTGAGCCGGAAGCGCGCTGCAGAGGGCGAGGCTCCAGTGGGGTCGGTTCGCGCATC 60
Db      |||||||
1 CCTGAGCCGGAAGCGCGCTGCAGAGGGCGAGGCTCCAGTGGGGTCGGTTCGCGCATC 60
QY      61 CAGCTAGCGTGTCCACGATCGCGTGGGCTCCGGGACTTTCGTACCTGTTGCGTAGCG 120
Db      |||||||
61 CAGCTAGCGTGTCCACGATCGCGTGGGCTCCGGGACTTTCGTACCTGTTGCGTAGCG 120
QY      121 ATCGAGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCGGGCTCCCGTTCGTTCC 180
Db      |||||||
121 ATCGAGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCGGGCTCCCGTTCGTTCC 180
QY      181 TCTGCCAGAGCGGAACACCGGAGCGGAGCCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
Db      |||||||
181 TCTGCCAGAGCGGAACACCGGAGCGGAGCCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
QY      241 TCTAACTGGACCAACGATCTCCACCTCTCTTCAAGTAAAGTTGTTATGTTCTGATAGAT 300
Db      |||||||
241 TCTAACTGGACCAACGATCTCCACCTCTCTTCAAGTAAAGTTGTTATGTTCTGATAGAT 300
QY      301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGGTGTGAATTTATGCCCTACACAACCT 360
Db      |||||||
301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGGTGTGAATTTATGCCCTACACAACCT 360
QY      361 TACCTTGTAAGAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAAGCCACCTACAGTT 420
Db      |||||||
361 TACCTTGTAAGAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAAGCCACCTACAGTT 420
QY      421 ACTATGCCTCGAATCAAGGCATTGATGACGGGAGCCCTTCCTGGCTTGTGCGACGTATC 480
Db      |||||||
421 ACTATGCCTCGAATCAAGGCATTGATGACGGGAGCCCTTCCTGGCTTGTGCGACGTATC 480
QY      481 AGGAACCTCAATTCTCCTGCACCTGCTGGAAGACAGTGTGATAAGCAAGCAAGCAAGCT 540
Db      |||||||
481 AGGAACCTCAATTCTCCTGCACCTGCTGGAAGACAGTGTGATAAGCAAGCAAGCAAGCT 540
QY      541 GGAAAAAGAAATAGTCTTTTATGGAGATGAAACCTGGGTTAAATATTATCCCAAAGCAATTT 600
Db      |||||||
541 GGAAAAAGAAATAGTCTTTTATGGAGATGAAACCTGGGTTAAATATTATCCCAAAGCAATTT 600
QY      601 GTGGAATATGATGGAACAACCTCATTTTCGTGTCAGATTACACAGAGGTGGATAATAAT 660
Db      |||||||
601 GTGGAATATGATGGAACAACCTCATTTTCGTGTCAGATTACACAGAGGTGGATAATAAT 660
QY      661 GTCACGAGGCATTGATATAAGTATTAAAAAGAGGAGATTGGGACATATTAAATCCTCCAC 720
Db      |||||||
661 GTCACGAGGCATTGATATAAGTATTAAAAAGAGGAGATTGGGACATATTAAATCCTCCAC 720
QY      721 TACCTGGGGCTGGACCAATTCGACATTTTTCAGGGCCCAACAGCCCCCTGATTGGGCAG 780
Db      |||||||
721 TACCTGGGGCTGGACCAATTCGACATTTTTCAGGGCCCAACAGCCCCCTGATTGGGCAG 780
QY      781 AAGCTGAGCGGAGATGGACAGCGTGTGATGAAGATCCACCTCACTGCAGTCGAAGGAG 840
Db      |||||||
781 AAGCTGAGCGGAGATGGACAGCGTGTGATGAAGATCCACCTCACTGCAGTCGAAGGAG 840
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Db      781 AAGCTGAGCGGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAG 840
QY      841 AGAGAGACGCTTTACCCAAATTTGCTGGTCTTGTGGTGACCATGGCATGTCTGAAACA 900
Db      |||||||
841 AGAGAGACGCTTTACCCAAATTTGCTGGTCTTGTGGTGACCATGGCATGTCTGAAACA 900
QY      901 GGAAGTCACGGGGCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT 960
Db      |||||||
901 GGAAGTCACGGGGCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT 960
QY      961 GCGTTTGAAGGAAACCCCGGTGATATCCGACATCCAAAGCACGTCCTCAATAGACGGATGTG 1020
Db      |||||||
961 GCGTTTGAAGGAAACCCCGGTGATATCCGACATCCAAAGCACGTCCTCAATAGACGGATGTG 1020
QY      1021 GCTGCGACACTGGCGATAGCATTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTC 1080
Db      |||||||
1021 GCTGCGACACTGGCGATAGCATTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTC 1080
QY      1081 CTATTTCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTTGAGATTTTACATTTGAAT 1140
Db      |||||||
1081 CTATTTCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTTGAGATTTTACATTTGAAT 1140
QY      1141 ACAGTCAGCTTAGTAACTGTGCAAGAGAATGTGCCGTCAATGAAAAAGATCCTGGG 1200
Db      |||||||
1141 ACAGTCAGCTTAGTAACTGTGCAAGAGAATGTGCCGTCAATGAAAAAGATCCTGGG 1200
QY      1201 TTTGAGCAGTTTAAATGTGAGAAAGATTGTCATGGGAACTGAGTGTACTTTGGAG 1260
Db      |||||||
1201 TTTGAGCAGTTTAAATGTGAGAAAGATTGTCATGGGAACTGAGTGTACTTTGGAG 1260
QY      1261 GAAAAGCATTCAGAACTCTATTCACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT 1320
Db      |||||||
1261 GAAAAGCATTCAGAACTCTATTCACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT 1320
QY      1321 GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGCCCGCAGTTCTCACCTGCTCC 1380
Db      |||||||
1321 GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGCCCGCAGTTCTCACCTGCTCC 1380
QY      1381 TGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGTGGAAAGTCCCACCTGTCACTC 1440
Db      |||||||
1381 TGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGTGGAAAGTCCCACCTGTCACTC 1440
QY      1441 CTGGGTTTCTCTGCTCTTTTATTTGGTGATCCTGGTCTTTTCGGCCGTTTCACTGCTATG 1500
Db      |||||||
1441 CTGGGTTTCTCTGCTCTTTTATTTGGTGATCCTGGTCTTTTCGGCCGTTTCACTGCTATG 1500
QY      1501 TGTGCACCTCAGCTGAAAGTTGCTGCTACTTCTGTGGCCTCTGTTGGTGGCGGAGGCT 1560
Db      |||||||
1501 TGTGCACCTCAGCTGAAAGTTGCTGCTACTTCTGTGGCCTCTGTTGGTGGCGGAGGCT 1560
QY      1561 GCCTTTGTTTACCAGACTCTGTTTGAACACCTGTTGTTGCCAAGTGTGCGCAGTGTCCC 1620
Db      |||||||
1561 GCCTTTGTTTACCAGACTCTGTTTGAACACCTGTTGTTGCCAAGTGTGCGCAGTGTCCC 1620
QY      1621 TGGACAGGGGGCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCCTCTGGGTGTCCC 1680
Db      |||||||
1621 TGGACAGGGGGCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCCTCTGGGTGTCCC 1680
QY      1681 GACACAGGTGTTCACTCTGTGCTGTGAGTCAAGTCAAGTCAAGTCTTGGAAAGCTAGGT 1740
Db      |||||||
1681 GACACAGGTGTTCACTCTGTGCTGTGAGTCAAGTCAAGTCAAGTCTTGGAAAGCTAGGT 1740
QY      1741 TCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGCGGTACAGAGGAACAAGCCCC 1800
Db      |||||||
1741 TCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGCGGTACAGAGGAACAAGCCCC 1800
QY      1801 CAGCTGAGGGGGTGTGTAATCGGACAGCCTCCACAGAGGTTGTGGGAGCTGCAGCTGA 1860
Db      |||||||
1801 CAGCTGAGGGGGTGTGTAATCGGACAGCCTCCACAGAGGTTGTGGGAGCTGCAGCTGA 1860
QY      1861 GGGAAAGAGAGACAATCGGCCTGGACACTCAGAGAGGTCAAAGGAGACTTGTGTCGACCC 1920
Db      |||||||
1861 GGGAAAGAGAGACAATCGGCCTGGACACTCAGAGAGGTCAAAGGAGACTTGTGTCGACCC 1920
```



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QY 1921 ACTCATCTGCCACCCCCAGAAATGATCGTGCCTCATCAGGTCAGATTTCTTTCCAAAG 1980
Db 1921 ACTCATCTGCCACCCCCAGAAATGATCGTGCCTCATCAGGTCAGATTTCTTTCCAAAG 1980
QY 1981 CGGACGTTTTCTGTTGGAATTTCTTAGTCTTGGCCTCGGACACCTTCATTCGTTAGCTGG 2040
Db 1981 CGGACGTTTTCTGTTGGAATTTCTTAGTCTTGGCCTCGGACACCTTCATTCGTTAGCTGG 2040
QY 2041 GGAGTGGTGTGAGGCAGTGAAGAAGAGGGGATGGTCACTCAGATCCACAGAGCCCA 2100
Db 2041 GGAGTGGTGTGAGGCAGTGAAGAAGAGGGGATGGTCACTCAGATCCACAGAGCCCA 2100
QY 2101 GGATCAAGGACCCACTGCAGTGGCAGCAGGACTGTTGGCCCCCCCCCAACCCCTGCAC 2160
Db 2101 GGATCAAGGACCCACTGCAGTGGCAGCAGGACTGTTGGCCCCCCCCCAACCCCTGCAC 2160
QY 2161 AGCCCTCATCCCTCTTGGCTTGAGCCGTGAGCCCTGAGTGTGCTGAGTGTGACCCGAGA 2220
Db 2161 AGCCCTCATCCCTCTTGGCTTGAGCCGTGAGCCCTGAGTGTGCTGAGTGTGACCCGAGA 2220
QY 2221 CACTCACAGCTTTGTGATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTGCCACG 2280
Db 2221 CACTCACAGCTTTGTGATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTGCCACG 2280
QY 2281 CTGACACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTTGAATTAGTACCTAG 2340
Db 2281 CTGACACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTTGAATTAGTACCTAG 2340
QY 2341 CTGCACACAGTATGTAGTTACCAAAAGATAAACCGSCAATAATTGAGAAAAAAA 2395
Db 2341 CTGCACACAGTATGTAGTTACCAAAAGATAAACCGSCAATAATTGAGAAAAAAA 2395
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RESULT 13

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US-10-063-554-139
; Sequence 139, Application US/10063554
; Publication No. US20030040013A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063, 554
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 139
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-554-139
```

```
Query Match 100.0%; Score 2395; DB 13; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGAGCGGAAGCGGGCTGCAGCAGGCGAGGCTCCAGGTGGGTCCGGTCCGCATC 60
Db 1 CCTGGAGCGGAAGCGGGCTGCAGCAGGCGAGGCTCCAGGTGGGTCCGGTCCGCATC 60
QY 61 CAGCCTAGCGTCCACGATCGGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCG 120
Db 61 CAGCCTAGCGTCCACGATCGGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCG 120
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QY 121 ATCAGGTCCTAGGATCGCGGTCTTCTTGGGGATTCTTCCGGCTCCCGTTCGTTCC 180
Db 121 ATCAGGTCCTAGGATCGCGGTCTTCTTGGGGATTCTTCCGGCTCCCGTTCGTTCC 180
QY 181 TCTGCCAGAGCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCTTCGGCTGGAGCCAGT 240
Db 181 TCTGCCAGAGCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCTTCGGCTGGAGCCAGT 240
QY 241 TCTAACTGGACACACGCTGCCACCACCTCTCTCTCAGTAAAGTTGTTATTGTTCTGATAGAT 300
Db 241 TCTAACTGGACACACGCTGCCACCACCTCTCTCTCAGTAAAGTTGTTATTGTTCTGATAGAT 300
QY 301 GCCTTGAGAGATGATTTTGTGTTTGGGTCAAAGGTTGTAATTTATGCCCTACACAACT 360
Db 301 GCCTTGAGAGATGATTTTGTGTTTGGGTCAAAGGTTGTAATTTATGCCCTACACAACT 360
QY 361 TACCTTGTGGAAGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAGCCACCTACAGTT 420
Db 361 TACCTTGTGGAAGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAGCCACCTACAGTT 420
QY 421 ACTATGCCTCGAATCAAGGCATTGATGACGGGAGCCCTTCTTGGCTTTGTGACGTCATC 480
Db 421 ACTATGCCTCGAATCAAGGCATTGATGACGGGAGCCCTTCTTGGCTTTGTGACGTCATC 480
QY 481 AGGAACCTCAATTCTCTCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAGAGCAGCT 540
Db 481 AGGAACCTCAATTCTCTCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAGAGCAGCT 540
QY 541 GGAAGAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTTAAATTTATCCAAAGCATTTT 600
Db 541 GGAAGAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTTAAATTTATCCAAAGCATTTT 600
QY 601 GTGGAATATGATGGAACAACCTCATTTTTCGTGTCAGATTACACAGAGGTGGATAATAAT 660
Db 601 GTGGAATATGATGGAACAACCTCATTTTTCGTGTCAGATTACACAGAGGTGGATAATAAT 660
QY 661 GTCACGAGGCATTTGGATAAAGTATTAAAGAGGAGATTGGGACATATTAAATCCTCCAC 720
Db 661 GTCACGAGGCATTTGGATAAAGTATTAAAGAGGAGATTGGGACATATTAAATCCTCCAC 720
QY 721 TACCTGGGGCTGGACCAATTGGCCACATTTTCAGGGCCCCAACAGCCCCCTGATTGGGCAG 780
Db 721 TACCTGGGGCTGGACCAATTGGCCACATTTTCAGGGCCCCAACAGCCCCCTGATTGGGCAG 780
QY 781 AAGCTGAGCGGATGGACAGCGTCTGATGAAGATCCACACCTCACTGCAGTCGAAGGAG 840
Db 781 AAGCTGAGCGGATGGACAGCGTCTGATGAAGATCCACACCTCACTGCAGTCGAAGGAG 840
QY 841 AGAGAGACGCTTTTACCCAAATTTGCTGGTTCTTTGTGTGACCATGGCATGTCTGAAACA 900
Db 841 AGAGAGACGCTTTTACCCAAATTTGCTGGTTCTTTGTGTGACCATGGCATGTCTGAAACA 900
QY 901 GGAAGTCACGGGGCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCT 960
Db 901 GGAAGTCACGGGGCTCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCT 960
QY 961 GCGTTTGAAGAGAAACCCCGTGATATCCGACATCCAAAGCACCTCCAATAGACGGATGTG 1020
Db 961 GCGTTTGAAGAGAAACCCCGTGATATCCGACATCCAAAGCACCTCCAATAGACGGATGTG 1020
QY 1021 GCTGCACACTGGCGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC 1080
Db 1021 GCTGCACACTGGCGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC 1080
QY 1081 CTATTCAGATTGTGGAAGGAAGCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
Db 1081 CTATTCAGATTGTGGAAGGAAGCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
QY 1141 ACAGTGCAGTTAGTAAACTGTTGCAAGAAATGTGCCGTCAATATGAAAAAGATCCTGGG 1200
Db 1141 ACAGTGCAGTTAGTAAACTGTTGCAAGAAATGTGCCGTCAATATGAAAAAGATCCTGGG 1200
QY 1201 TTTGAGCAGTTTAAATGTCAAGAAAGATTGTCATGGGAACCTGGATCAGACTGTACTGGAG 1260
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	Db	181	TCTGCCAGACGGAAACA CGGAGCGGAGCCCCCAGCGCCGAAACCCTCGGCTGGAGCCAGT	240
	QY	241	TCTAACTGGACCACGCTGCCACCACTCTCTTTTCAGTAAAGTGTTATTGTCTCTGATAGAT	300
	Db	241	TCTAACTGGACCACGCTGCCACCACTCTCTTTTCAGTAAAGTGTTATTGTCTGATAGAT	300
	QY	301	GCCTTGAGAGATGATTTTGTGTTTTGGGTCAAAGGGGTGTGAATAATTATGCCCTACACAAC	360
	Db	301	GCCTTGAGAGATGATTTTGTGTTTTGGGTCAAAGGGGTGTGAATAATTATGCCCTACACAAC	360
	QY	361	TACCTTGTTGAAAAAAGGAGCATCTCACAGTTTTTGTGGCTGAAGCAAAAGCCACCTACAGTT	420
	Db	361	TACCTTGTTGAAAAAAGGAGCATCTCACAGTTTTTGTGGCTGAAGCAAAAGCCACCTACAGTT	420
	QY	421	ACTATGCCCTCGAATCAAGGCATTGATGACGGGAGCCCTTCCTGGCTTTGTTCGACGTCATC	480
	Db	421	ACTATGCCCTCGAATCAAGGCATTGATGACGGGAGCCCTTCCTGGCTTTGTTCGACGTCATC	480
	QY	481	AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGACAAAGCAAAAGCAGCT	540
	Db	481	AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGACAAAGCAAAAGCAGCT	540
	QY	541	GGA AAAAGAATAGTCTTTTATGGAGATGAAAACCTGGTTAAATTAATTTCCAAAGCATTTT	600
	Db	541	GGA AAAAGAATAGTCTTTTATGGAGATGAAAACCTGGTTAAATTAATTTCCAAAGCATTTT	600
	QY	601	GTGGAATATGATGGAACAACCTCATTTTTCGTCTCAGATTACACAGAGCTGGATAATAAT	660
	Db	601	GTGGAATATGATGGAACAACCTCATTTTTCGTCTCAGATTACACAGAGCTGGATAATAAT	660
	QY	661	GTACAGAGGCATTTGGATAAAGTATTA AAAAGAGAGATTGGGACATATTAATCCTCCAC	720
	Db	661	GTACAGAGGCATTTGGATAAAGTATTA AAAAGAGAGATTGGGACATATTAATCCTCCAC	720
	QY	721	TACCTGGGGCTGGACCAACATTTGGCCACATTTACGGGCCCACACAGCCCCTGATTGGGCAG	780
	Db	721	TACCTGGGGCTGGACCAACATTTGGCCACATTTACGGGCCCACACAGCCCCTGATTGGGCAG	780
	QY	781	AAGCTGACGAGATGGACACGCTGCTGATGAAGATCCACACCTCAGTCAGTCGAAGGAG	840
	Db	781	AAGCTGACGAGATGGACACGCTGCTGATGAAGATCCACACCTCAGTCAGTCGAAGGAG	840
	QY	841	AGAGAGACGCCCTTACCCAATTTGCTGGTTCTTTTGTGGTGACCATGGCATCTCTGAAACA	900
	Db	841	AGAGAGACGCCCTTACCCAATTTGCTGGTTCTTTTGTGGTGACCATGGCATCTCTGAAACA	900
	QY	901	GGAGTCACGGGGCCTCCTCCACCGAGGAGTGAATACACCTCTGATTTTAAATCAGTTCT	960
	Db	901	GGAGTCACGGGGCCTCCTCCACCGAGGAGTGAATACACCTCTGATTTTAAATCAGTTCT	960
	QY	961	GC GTTTGAAAAGGAAACCCCGGTGATATCCGACATCCAAAGCAGTCCAATAGACGGATGTG	1020
	Db	961	GC GTTTGAAAAGGAAACCCCGGTGATATCCGACATCCAAAGCAGTCCAATAGACGGATGTG	1020
	QY	1021	GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTAGGAGCCTC	1080
	Db	1021	GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTAGGAGCCTC	1080
	QY	1081	CTATTTCCCAAGTTGTGGAAGGAAGCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT	1140
	Db	1081	CTATTTCCCAAGTTGTGGAAGGAAGCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT	1140
	QY	1141	ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAAATGTGCCGTGATATGAAAAGATCCTGGG	1200
	Db	1141	ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAAATGTGCCGTGATATGAAAAGATCCTGGG	1200
	QY	1201	TTTGAGCAGTTTAAAATGT CAGAAAGATTGCATGGGAACCTGGATCAGACTGTACTTGGAG	1260
	Db	1201	TTTGAGCAGTTTAAAATGT CAGAAAGATTGCATGGGAACCTGGATCAGACTGTACTTGGAG	1260
	QY	1261	GA AAAGCATTCAGAAAGTCCATTCAACCTGGGCTCCAAAGTTCTCAGGCAGTACCTGGAT	1320

RESULT 15

US-10-305-654-291
; Sequence 291, Application US/10305654
; Publication No. US20030224984A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hans-Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, J.
; APPLICANT: Paoni, N. F.
; APPLICANT: Stephan, J-P F.
; APPLICANT: Watanabe, C.K.
; APPLICANT: Wood, W.I.
; APPLICANT: Williams, P.M.
; APPLICANT: Ye, Weilan

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235R1C1
; CURRENT APPLICATION NUMBER: US/10/305,654
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 291

; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homosapiens
US-10-305-654-291

Query Match		100.0%;	Score 2395;	DB 13;	Length 2395;	
Best Local Similarity		100.0%;	Pred. No. 0;			
Matches 2395;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	CCTGGAGCCGGAAGCGGCTGCAGAGCGGAGGCTCCAGGTGGGTCGGTTC	CGCATC	60		
Db	1	CCTGGAGCCGGAAGCGGCTGCAGAGCGGAGGCTCCAGGTGGGTCGGTTC	CGCATC	60		
QY	61	CAGCCTAGCGTGTCCACGATGCGGCTGGGCTCCGGGACCTTCGCTACCTGTTCG	TAGCG	120		
Db	61	CAGCCTAGCGTGTCCACGATGCGGCTGGGCTCCGGGACCTTCGCTACCTGTTCG	TAGCG	120		
QY	121	ATCGAGTGTAGGGATCGCGGTCTTCCTTCGGGGATCTTCGCGGCTCCCGTTCG	TTCC	180		
Db	121	ATCGAGTGTAGGGATCGCGGTCTTCCTTCGGGGATCTTCGCGGCTCCCGTTCG	TTCC	180		
QY	181	TCTGCCAGAGCGGAACACGAGCGGAGCCCCCAGCGCCCCGACCCCTCGGCTGG	AGCCAGT	240		
Db	181	TCTGCCAGAGCGGAACACGAGCGGAGCCCCCAGCGCCCCGACCCCTCGGCTGG	AGCCAGT	240		
QY	241	TCTAACTGGACCAACGCTGCCACCACTCTCTTCAGTAAAGTTGTTATGTTCTG	ATAGAT	300		
Db	241	TCTAACTGGACCAACGCTGCCACCACTCTCTTCAGTAAAGTTGTTATGTTCTG	ATAGAT	300		
QY	301	GCCTTGAGAGATGATTTTGTGTTTGGGTCAAAGGTGTGAATTTATGCCCTAC	CAACT	360		
Db	301	GCCTTGAGAGATGATTTTGTGTTTGGGTCAAAGGTGTGAATTTATGCCCTAC	CAACT	360		
QY	361	TACCTTGTGGAAGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAAGCCAC	TACAGTT	420		
Db	361	TACCTTGTGGAAGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAAGCCAC	TACAGTT	420		
QY	421	ACTATGCCCTCGAATCAAGGCATGATGACGGGAGCCCTTCCTGGCTTTGTCG	ACGTATC	480		
Db	421	ACTATGCCCTCGAATCAAGGCATGATGACGGGAGCCCTTCCTGGCTTTGTCG	ACGTATC	480		
QY	481	AGGAACCTCAATTCTCCTGCACCTGCTGGAAGACAGTGTGATAAGACAAGCA	AGCAGCT	540		
Db						

Db	481	AGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAGCAGCT	540
QY	541	GGAAAAAGAAATAGTCTTTTATGAGATGAAACCTGGGTTAAATATTATCCAAAGCATTTT	600
Db	541	GGAAAAAGAAATAGTCTTTTATGAGATGAAACCTGGGTTAAATATTATCCAAAGCATTTT	600
QY	601	GTGGAATATGATGGAACACCTCATTTTTCGTGTCAGATTACAGAGGTGGATAATAAT	660
Db	601	GTGGAATATGATGGAACACCTCATTTTTCGTGTCAGATTACAGAGGTGGATAATAAT	660
QY	661	GTCACGAGGCATTTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAAATCCTCCAC	720
Db	661	GTCACGAGGCATTTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAAATCCTCCAC	720
QY	721	TACCTGGGCTGGACCAATTTGGCCACATTTTACGGGCCCAACAGCCCCCTGATTGGGAG	780
Db	721	TACCTGGGCTGGACCAATTTGGCCACATTTTACGGGCCCAACAGCCCCCTGATTGGGAG	780
QY	781	AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAG	840
Db	781	AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAG	840
QY	841	AGAGAGACGCTTTTACCCAAATTTGCTGGTTCCTTGTGGTGACCATGGCATGTCTGAAACA	900
Db	841	AGAGAGACGCTTTTACCCAAATTTGCTGGTTCCTTGTGGTGACCATGGCATGTCTGAAACA	900
QY	901	GGAAGTCACGGGGCTCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT	960
Db	901	GGAAGTCACGGGGCTCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT	960
QY	961	CGGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGCACGTCCAAATAGACGGATGTG	1020
Db	961	CGGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGCACGTCCAAATAGACGGATGTG	1020
QY	1021	GCTGCGACACTGGCGATAGCACCTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC	1080
Db	1021	GCTGCGACACTGGCGATAGCACCTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC	1080
QY	1081	CTATTCACAGTTGTGGAAGGAAGACCAATGAGAGACAGTGTGAGATTTTACATTTGAAT	1140
Db	1081	CTATTCACAGTTGTGGAAGGAAGACCAATGAGAGACAGTGTGAGATTTTACATTTGAAT	1140
QY	1141	ACAGTGCAGCTTAGTAACTGTTGCAAGAGAATGTGCCGTCAATGAAAAAGATCCTGGG	1200
Db	1141	ACAGTGCAGCTTAGTAACTGTTGCAAGAGAATGTGCCGTCAATGAAAAAGATCCTGGG	1200
QY	1201	TTTGTGACAGTTTAAATGTCAGAAAGATTGCATGGGAACCTGAGTCAGACTGTACTTGGAG	1260
Db	1201	TTTGTGACAGTTTAAATGTCAGAAAGATTGCATGGGAACCTGAGTCAGACTGTACTTGGAG	1260
QY	1261	GAAAGCATTCAGAACTCTTATCAACCTGGGCTCCAAGTTCTCAGGCAGTACCTGGAT	1320
Db	1261	GAAAGCATTCAGAACTCTTATCAACCTGGGCTCCAAGTTCTCAGGCAGTACCTGGAT	1320
QY	1321	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGCGCCAGTTCTCACCCCTGCTCC	1380
Db	1321	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGCGCCAGTTCTCACCCCTGCTCC	1380
QY	1381	TGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACCTGTCACTC	1440
Db	1381	TGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACCTGTCACTC	1440
QY	1441	CTGGGTTTCTCTGCTCTTTTATTTGGTGATCCTGGTCTTTTCGGCCGTTTCAAGTATG	1500
Db	1441	CTGGGTTTCTCTGCTCTTTTATTTGGTGATCCTGGTCTTTTCGGCCGTTTCAAGTATG	1500
QY	1501	TGTGCACCTCAGCTGAAAGTTTCTGCTACTTTTGTGGCTCTCTCGTGGCTGGCGCAGGCT	1560
Db	1501	TGTGCACCTCAGCTGAAAGTTTCTGCTACTTTTGTGGCTCTCTCGTGGCTGGCGCAGGCT	1560
QY	1561	GCCTTTTCCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCC	1620
Db	1561	GCCTTTTCCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCC	1620

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QY	1621	TGGACAGGGGGCTCAGGGAAGGACGTGAGCAGCCTTATCCAGGCTCTGGGTGTCCC	1680
Db	1621	TGGACAGGGGGCTCAGGGAAGGACGTGAGCAGCCTTATCCAGGCTCTGGGTGTCCC	1680
QY	1681	GACACAGGTGTTACATCTGTGCTGTCAAGTCAGATGCCCTCAGTTCTTGGAAAGCTAGGT	1740
Db	1681	GACACAGGTGTTACATCTGTGCTGTCAAGTCAGATGCCCTCAGTTCTTGGAAAGCTAGGT	1740
QY	1741	TCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAAACAAGCCCCC	1800
Db	1741	TCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAAACAAGCCCCC	1800
QY	1801	CAGCTGAGGGGTGTGTGAATCGGACAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGA	1860
Db	1801	CAGCTGAGGGGTGTGTGAATCGGACAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGA	1860
QY	1861	GGGAAGAAGAGACAATCGGCTGGACACTCAGGAGGTCAAAAGGAGACTTGGTCGCACC	1920
Db	1861	GGGAAGAAGAGACAATCGGCTGGACACTCAGGAGGTCAAAAGGAGACTTGGTCGCACC	1920
QY	1921	ACTCATCCTGCCACCCCAAGATGCATCCTGCCTCATCAGTCCAGATTCTTTCCAAAG	1980
Db	1921	ACTCATCCTGCCACCCCAAGATGCATCCTGCCTCATCAGTCCAGATTCTTTCCAAAG	1980
QY	1981	CGGACGTTTTCTGTTGGAAATTTAGTCCTTGGCCTCGGACACCTTCATTGTTAGCTGG	2040
Db	1981	CGGACGTTTTCTGTTGGAAATTTAGTCCTTGGCCTCGGACACCTTCATTGTTAGCTGG	2040
QY	2041	GGAGTGGTGGTGAGGCAAGTGAAGAAGAGGGGATGGTCACACTCAGATCCACAGAGCCCA	2100
Db	2041	GGAGTGGTGGTGAGGCAAGTGAAGAAGAGGGGATGGTCACACTCAGATCCACAGAGCCCA	2100
QY	2101	GGATCAAGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCACCCCTGCAC	2160
Db	2101	GGATCAAGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCACCCCTGCAC	2160
QY	2161	AGCCCTCATCCCTCTTGGCTTGAGCCGTGAGAGGCCCCCTGTGCTGAGTGTCTGACCGAGA	2220
Db	2161	AGCCCTCATCCCTCTTGGCTTGAGCCGTGAGAGGCCCCCTGTGCTGAGTGTCTGACCGAGA	2220
QY	2221	CACTCACAGCTTTGTTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACG	2280
Db	2221	CACTCACAGCTTTGTTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACG	2280
QY	2281	CTTGCACTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG	2340
Db	2281	CTTGCACTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG	2340
QY	2341	CTGCACACAGTATGTAGTTACCAAGAAATAACGGCAATAATTGAGAAAAAAA	2395
Db	2341	CTGCACACAGTATGTAGTTACCAAGAAATAACGGCAATAATTGAGAAAAAAA	2395

Search completed: August 5, 2004, 22:54:35
Job time : 1097 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2004, 17:39:35 ; Search time 193 Seconds
(without alignments)
6886.567 Million cell updates/sec

Title: US-10-036-150-44
Perfect score: 2395
Sequence: 1 cctggagcgcgaagcgccgc.....gcaataattgagaaaaaa 2395

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	53	2.2	578	4	US-09-621-976-252
2	42	1.8	7218	1	US-08-232-463-14
3	39.6	1.7	7218	1	US-08-232-463-14
4	38.8	1.6	832	4	US-09-621-976-2813
5	37.4	1.6	2527	4	US-09-555-790A-1
6	37	1.5	458	3	US-09-141-000-4
7	37	1.5	505	4	US-09-621-976-15639
8	36.8	1.5	969	4	US-09-489-039A-2802
9	36.8	1.5	1033	4	US-09-610-185C-3
10	36.6	1.5	364	4	US-09-621-976-17202
11	36.6	1.5	2480	4	US-09-023-655-1096
12	36.2	1.5	77536	4	US-09-410-551B-1
13	35.4	1.5	17000	4	US-09-679-299A-18
14	35.4	1.5	118067	4	US-09-497-855A-32
15	35.2	1.5	444	4	US-09-252-991A-12919
16	35.2	1.5	882	4	US-09-252-991A-12566
17	35.2	1.5	918	4	US-08-956-171E-513
18	35.2	1.5	1224	4	US-09-252-991A-13240
19	35.2	1.5	1422	4	US-09-252-991A-13065
20	35.2	1.5	1485	4	US-09-252-991A-12874
21	35.2	1.5	1528	4	US-09-016-434-1448
22	35.2	1.5	1659	1	US-08-333-358-7
23	35.2	1.5	1659	1	US-08-463-694-7
24	35.2	1.5	1659	1	US-08-694-501-7
25	35.2	1.5	3001	4	US-09-539-333D-185
26	35	1.5	2150	3	US-09-263-023-1
27	35	1.5	2150	4	US-09-471-867-1
					Sequence 252, App
					Sequence 14, Appl
					Sequence 14, Appl
					Sequence 2813, Ap
					Sequence 1, Appli
					Sequence 4, Appli
					Sequence 15639, A
					Sequence 2802, Ap
					Sequence 3, Appli
					Sequence 17202, A
					Sequence 1096, Ap
					Sequence 1, Appli
					Sequence 18, Appl
					Sequence 32, Appl
					Sequence 12919, A
					Sequence 12566, A
					Sequence 513, App
					Sequence 13240, A
					Sequence 13065, A
					Sequence 12874, A
					Sequence 1448, Ap
					Sequence 7, Appli
					Sequence 7, Appli
					Sequence 7, Appli
					Sequence 185, App
					Sequence 1, Appli
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c 28	1.5	2433	4	US-09-328-352-3055	Sequence 3055, Ap
c 29	1.5	618	4	US-09-252-991A-1668	Sequence 1668, Ap
c 30	1.5	702	4	US-09-252-991A-1447	Sequence 1447, Ap
c 31	1.5	1038	4	US-09-252-991A-1505	Sequence 1505, Ap
c 32	1.5	1539	4	US-09-023-655-62	Sequence 62, Appl
c 33	1.5	1956	4	US-09-976-594-253	Sequence 253, App
c 34	1.5	2061	4	US-09-252-991A-1544	Sequence 1544, Ap
c 35	1.5	2148	4	US-09-489-039A-5340	Sequence 5340, Ap
c 36	1.5	3651	2	US-08-790-374-1	Sequence 1, Appli
c 37	1.4	2614	4	US-09-004-056-1	Sequence 1, Appli
c 38	1.4	123025	4	US-09-198-452A-1	Sequence 1, Appli
c 39	1.4	1425	4	US-09-489-039A-2465	Sequence 2465, Ap
c 40	1.4	1548	4	US-09-170-496D-219	Sequence 219, App
c 41	1.4	832	4	US-09-621-976-2813	Sequence 2813, Ap
c 42	1.4	364	4	US-09-621-976-17202	Sequence 17202, A
c 43	1.4	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c 44	1.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 45	1.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 46	1.4	418	3	US-09-141-000-6	Sequence 6, Appli
c 47	1.4	1230	4	US-09-252-991A-14979	Sequence 14979, A
c 48	1.4	3045	4	US-09-252-991A-14767	Sequence 14767, A
c 49	1.4	5330	4	US-09-023-905A-1	Sequence 1, Appli
c 50	1.4	1065	4	US-08-976-063E-3	Sequence 3, Appli
c 51	1.4	1140	4	US-09-252-991A-10867	Sequence 10867, A
c 52	1.4	1398	4	US-09-252-991A-10813	Sequence 10813, A
c 53	1.4	32679	4	US-08-976-063E-1	Sequence 1, Appli
c 54	1.4	255	4	US-09-489-039A-5337	Sequence 5337, Ap
c 55	1.4	421	4	US-09-621-976-18671	Sequence 18671, A
c 56	1.4	511	4	US-09-679-409-71	Sequence 71, Appl
c 57	1.4	3001	4	US-09-539-333D-145	Sequence 145, App
c 58	1.4	4214	4	US-09-221-017B-293	Sequence 293, App
c 59	1.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 60	1.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 61	1.4	390	4	US-09-252-991A-5733	Sequence 5733, Ap
c 62	1.4	511	4	US-09-144-428-14	Sequence 14, Appl
c 63	1.4	708	4	US-09-144-428-9	Sequence 9, Appli
c 64	1.4	834	4	US-09-621-976-2574	Sequence 2574, Ap
c 65	1.4	879	4	US-09-252-991A-5693	Sequence 5693, Ap
c 66	1.4	2115	4	US-09-252-991A-5749	Sequence 5749, Ap
c 67	1.4	2160	4	US-09-252-991A-5707	Sequence 5707, Ap
c 68	1.4	1548	4	US-09-170-496D-103	Sequence 103, App
c 69	1.4	6854	4	US-09-194-905-7	Sequence 7, Appli
c 70	1.4	600	4	US-09-328-352-3094	Sequence 3094, Ap
c 71	1.4	989	4	US-09-833-381-990	Sequence 990, App
c 72	1.4	1013	4	US-08-930-830B-1	Sequence 1, Appli
c 73	1.4	6152	1	US-08-557-139-1	Sequence 1, Appli
c 74	1.4	9208	4	US-09-068-506-1	Sequence 1, Appli
c 75	1.4	50000	4	US-09-146-053-4	Sequence 4, Appli
c 76	1.4	58407	4	US-08-916-421B-2	Sequence 2, Appli
c 77	1.3	444	4	US-09-489-039A-3299	Sequence 3299, Ap
c 78	1.3	1386	4	US-09-134-000C-703	Sequence 703, App
c 79	1.3	4235	4	US-09-620-312D-380	Sequence 380, App
c 80	1.3	5361	3	US-08-973-462-2	Sequence 2, Appli
c 81	1.3	6152	3	US-08-973-462-1	Sequence 1, Appli
c 82	1.3	289	3	US-09-007-005-17	Sequence 17, Appl
c 83	1.3	289	3	US-09-244-796-17	Sequence 17, Appl
c 84	1.3	543	4	US-09-134-000C-1206	Sequence 1206, Ap
c 85	1.3	647	4	US-09-023-655-790	Sequence 790, App
c 86	1.3	738	4	US-09-182-145-38	Sequence 38, Appl
c 87	1.3	841	4	US-09-182-145-39	Sequence 39, Appl
c 88	1.3	861	2	US-08-924-759-15	Sequence 15, Appl
c 89	1.3	861	3	US-09-248-335-15	Sequence 15, Appl
c 90	1.3	1279	3	US-09-248-335-25	Sequence 25, Appl
c 91	1.3	1293	4	US-09-182-145-13	Sequence 13, Appl
c 92	1.3	1293	4	US-09-182-145-14	Sequence 14, Appl
c 93	1.3	1893	3	US-08-878-474-10	Sequence 10, Appl
c 94	1.3	2039	3	US-09-276-531-45	Sequence 45, Appl
c 95	1.3	2039	4	US-09-976-594-478	Sequence 478, App
c 96	1.3	4320	4	US-09-543-681A-3388	Sequence 3388, Ap
c 97	1.3	5319	2	US-08-861-464-7	Sequence 7, Appli
c 98	1.3	5319	2	US-08-396-001-7	Sequence 7, Appli
c 99	1.3	5319	3	US-09-323-433A-7	Sequence 7, Appli
c 100	1.3	6755	3	US-08-931-999-4	Sequence 4, Appli

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C 101	32	1.3	32207	2	US-08-770-379-20	Sequence 20, Appl	174	31.2	1.3	2655	2	US-08-470-566B-26	Sequence 26, Appl
C 102	32	1.3	32207	3	US-08-757-669A-20	Sequence 20, Appl	175	31.2	1.3	2655	2	US-08-469-334-17	Sequence 17, Appl
C 103	32	1.3	32207	4	US-09-230-371A-20	Sequence 20, Appl	176	31.2	1.3	2655	2	US-08-469-334-26	Sequence 26, Appl
104	32	1.3	35100	2	US-08-770-379-17	Sequence 17, Appl	177	31.2	1.3	2655	3	US-09-300-529-17	Sequence 17, Appl
105	32	1.3	35100	3	US-08-757-669A-17	Sequence 17, Appl	178	31.2	1.3	2655	3	US-09-300-529-26	Sequence 26, Appl
106	32	1.3	35100	4	US-09-230-371A-17	Sequence 17, Appl	179	31.2	1.3	4031	1	US-08-471-033-49	Sequence 49, Appl
107	32	1.3	580073	4	US-08-545-528D-1	Sequence 1, Appl	180	31.2	1.3	4031	2	US-08-471-044-49	Sequence 49, Appl
108	31.8	1.3	543	4	US-09-134-000C-344	Sequence 344, App	181	31.2	1.3	4031	2	US-08-463-483A-49	Sequence 49, Appl
109	31.8	1.3	1001	4	US-09-641-638-163	Sequence 163, App	182	31.2	1.3	4031	2	US-08-471-046A-49	Sequence 49, Appl
C 110	31.8	1.3	1173	3	US-09-414-010-1	Sequence 1, Appl	183	31.2	1.3	4031	2	US-08-470-566B-49	Sequence 49, Appl
C 111	31.8	1.3	1173	4	US-09-812-216-1	Sequence 1, Appl	184	31.2	1.3	4031	3	US-08-469-334-49	Sequence 49, Appl
C 112	31.8	1.3	1788	4	US-09-628-188A-1	Sequence 6262, Ap	185	31.2	1.3	4079	4	US-09-016-434-1246	Sequence 1246, Ap
C 113	31.8	1.3	5727	4	US-09-614-770A-1	Sequence 1, Appl	186	31.2	1.3	4141	4	US-09-245-281-42	Sequence 42, Appl
C 114	31.8	1.3	49272	1	US-08-621-976-16656	Sequence 1, Appl	187	31.2	1.3	4141	4	US-09-207-359B-42	Sequence 42, Appl
C 115	31.6	1.3	430	4	US-09-010-147B-13	Sequence 13, Appl	188	31.2	1.3	4141	4	US-09-340-620A-42	Sequence 42, Appl
C 116	31.6	1.3	582	4	US-09-671-317-251	Sequence 251, App	189	31.2	1.3	4141	4	US-09-865-364-42	Sequence 42, Appl
C 117	31.6	1.3	984	4	US-09-484-970B-28	Sequence 28, Appl	190	31.2	1.3	4242	4	US-09-023-655-1201	Sequence 1201, Ap
C 118	31.6	1.3	2235	4	US-09-620-312D-12	Sequence 12, Appl	191	31.2	1.3	4796	3	US-09-085-199B-3	Sequence 3, Appl
C 119	31.6	1.3	2243	4	US-09-081-385-10	Sequence 10, Appl	192	31.2	1.3	11558	5	PCT-US93-06251-23	Sequence 23, Appl
C 120	31.6	1.3	3306	4	US-09-593-580B-1	Sequence 1, Appl	193	31.2	1.3	29629	4	US-09-729-995-3	Sequence 3, Appl
C 121	31.6	1.3	9464	4	US-08-776-971-2	Sequence 2, Appl	194	31.2	1.3	29629	4	US-10-135-689-3	Sequence 3, Appl
C 122	31.4	1.3	294	3	US-08-828-451-7	Sequence 7, Appl	195	31.2	1.3	469	3	US-09-085-199B-29	Sequence 29, Appl
C 123	31.4	1.3	380	3	US-08-828-451-114	Sequence 114, App	196	31	1.3	726	4	US-09-252-991A-6538	Sequence 6538, Ap
C 124	31.4	1.3	380	3	US-08-776-971-116	Sequence 116, App	197	31	1.3	852	4	US-09-252-991A-2774	Sequence 2774, Ap
C 125	31.4	1.3	885	4	US-08-134-000C-1319	Sequence 1319, Ap	198	31	1.3	1521	4	US-09-252-991A-6495	Sequence 6495, Ap
C 126	31.4	1.3	1117	2	US-08-960-022-1	Sequence 1, Appl	199	31	1.3	1575	4	US-09-252-991A-3100	Sequence 3100, Ap
C 127	31.4	1.3	1358	4	US-09-023-655-84	Sequence 84, Appl	200	31	1.3	1956	4	US-09-252-991A-3189	Sequence 3189, Ap
C 128	31.4	1.3	1473	2	US-08-541-033A-25	Sequence 25, Appl	201	31	1.3	3889	4	US-09-484-970B-39	Sequence 39, Appl
C 129	31.4	1.3	1473	2	US-08-828-451-25	Sequence 25, Appl	202	31	1.3	3898	4	US-09-268-866-1	Sequence 1, Appl
C 130	31.4	1.3	1506	2	US-08-541-033A-23	Sequence 23, Appl	203	31	1.3	4098	4	US-09-620-312D-351	Sequence 351, App
C 131	31.4	1.3	1506	2	US-08-828-451-23	Sequence 23, Appl	204	31	1.3	5238	4	US-09-221-017B-173	Sequence 173, App
C 132	31.4	1.3	1969	2	US-08-541-033A-7	Sequence 7, Appl	205	31	1.3	7012	4	US-09-732-025-3	Sequence 3, Appl
C 133	31.4	1.3	1969	2	US-08-828-451-7	Sequence 7, Appl	206	31	1.3	8285	4	US-09-739-455-3	Sequence 3, Appl
C 134	31.4	1.3	2096	2	US-08-541-033A-19	Sequence 19, Appl	207	31	1.3	11827	4	US-09-739-455-3	Sequence 4438, Ap
C 135	31.4	1.3	2096	2	US-08-828-451-19	Sequence 19, Appl	208	30.8	1.3	297	4	US-09-313-294A-4438	Sequence 907, App
C 136	31.4	1.3	2099	2	US-08-541-033A-3	Sequence 3, Appl	209	30.8	1.3	581	4	US-09-833-381-907	Sequence 22, Appl
C 137	31.4	1.3	2099	2	US-08-828-451-3	Sequence 3, Appl	210	30.8	1.3	896	4	US-09-404-879A-22	Sequence 22, Appl
C 138	31.4	1.3	2137	2	US-08-541-033A-18	Sequence 18, Appl	211	30.8	1.3	896	4	US-09-338-933-22	Sequence 22, Appl
C 139	31.4	1.3	2137	2	US-08-828-451-18	Sequence 18, Appl	212	30.8	1.3	896	4	US-09-215-681-22	Sequence 22, Appl
C 140	31.4	1.3	2140	2	US-08-541-033A-1	Sequence 1, Appl	213	30.8	1.3	896	4	US-09-216-003A-22	Sequence 22, Appl
C 141	31.4	1.3	2140	2	US-08-828-451-1	Sequence 1, Appl	214	30.8	1.3	1269	4	US-09-107-532A-1803	Sequence 1803, Ap
C 142	31.4	1.3	3117	3	US-08-909-954-3	Sequence 3, Appl	215	30.8	1.3	3226	1	US-07-862-021B-11	Sequence 11, Appl
C 143	31.4	1.3	13067	3	US-09-356-952-12	Sequence 5, Appl	216	30.8	1.3	3226	1	US-08-313-288B-11	Sequence 11, Appl
C 144	31.4	1.3	43676	3	US-09-740-041-3	Sequence 12, Appl	217	30.8	1.3	3226	5	PCT-US93-03164-11	Sequence 11, Appl
C 145	31.4	1.3	66804	4	US-09-596-002-36	Sequence 36, Appl	218	30.8	1.3	3772	4	US-09-962-665-5	Sequence 5, Appl
C 146	31.4	1.3	92407	4	US-09-596-002-36	Sequence 36, Appl	219	30.8	1.3	3772	4	US-09-963-333-5	Sequence 5, Appl
C 147	31.2	1.3	1164	3	US-09-085-199B-1	Sequence 1, Appl	220	30.8	1.3	4032	1	US-08-107-748-3	Sequence 3, Appl
C 148	31.2	1.3	1331	4	US-09-023-655-579	Sequence 579, App	221	30.8	1.3	4032	1	US-08-245-809-4	Sequence 4, Appl
C 149	31.2	1.3	2004	1	US-08-471-033-18	Sequence 18, Appl	222	30.8	1.3	4032	5	PCT-US92-01385-3	Sequence 3, Appl
150	31.2	1.3	2004	2	US-08-471-044-18	Sequence 18, Appl	223	30.8	1.3	10482	4	US-09-322-478-23	Sequence 23, Appl
151	31.2	1.3	2004	2	US-08-463-483A-18	Sequence 18, Appl	224	30.8	1.3	11131	4	US-10-204-708-27	Sequence 27, Appl
152	31.2	1.3	2004	2	US-08-471-046A-18	Sequence 18, Appl	225	30.8	1.3	11131	4	US-08-785-150-1	Sequence 1, Appl
153	31.2	1.3	2004	2	US-08-470-566B-18	Sequence 18, Appl	226	30.8	1.3	14507	4	US-09-660-299-1	Sequence 1, Appl
154	31.2	1.3	2004	2	US-08-469-334-18	Sequence 18, Appl	227	30.8	1.3	14507	4	US-09-435-377-1	Sequence 1, Appl
155	31.2	1.3	2004	2	US-09-300-529-18	Sequence 18, Appl	228	30.8	1.3	14507	4	US-09-973-928-1	Sequence 1, Appl
156	31.2	1.3	2310	4	US-09-134-000C-1714	Sequence 1714, Ap	229	30.8	1.3	35524	3	US-08-923-137-1	Sequence 1, Appl
C 157	31.2	1.3	2547	4	US-09-765-298A-9	Sequence 9, Appl	230	30.6	1.3	288	1	US-08-157-171-8	Sequence 8, Appl
158	31.2	1.3	2576	1	US-08-471-033-35	Sequence 35, Appl	231	30.6	1.3	297	3	US-08-776-971-120	Sequence 120, App
159	31.2	1.3	2576	2	US-08-471-044-35	Sequence 35, Appl	232	30.6	1.3	297	3	US-08-776-971-121	Sequence 121, App
160	31.2	1.3	2576	2	US-08-463-483A-35	Sequence 35, Appl	233	30.6	1.3	380	3	US-08-776-971-132	Sequence 132, App
161	31.2	1.3	2576	2	US-08-471-046A-35	Sequence 35, Appl	234	30.6	1.3	474	4	US-09-621-976-18033	Sequence 18033, A
162	31.2	1.3	2576	2	US-08-469-334-35	Sequence 35, Appl	235	30.6	1.3	537	4	US-09-252-991A-13469	Sequence 2720, Ap
163	31.2	1.3	2576	2	US-08-470-566B-35	Sequence 35, Appl	236	30.6	1.3	714	4	US-09-489-039A-2720	Sequence 118, App
164	31.2	1.3	2576	2	US-08-469-334-35	Sequence 35, Appl	237	30.6	1.3	769	3	US-08-776-971-118	Sequence 119, App
165	31.2	1.3	2655	1	US-08-471-033-17	Sequence 17, Appl	238	30.6	1.3	1189	2	US-08-450-042A-2	Sequence 2, Appl
166	31.2	1.3	2655	2	US-08-471-033-26	Sequence 26, Appl	239	30.6	1.3	1218	4	US-09-894-844-109	Sequence 109, Appl
167	31.2	1.3	2655	2	US-08-471-044-26	Sequence 17, Appl	240	30.6	1.3	1856	3	US-08-157-171-3	Sequence 3, Appl
168	31.2	1.3	2655	2	US-08-463-483A-17	Sequence 26, Appl	241	30.6	1.3	1856	3	US-09-050-159-128	Sequence 128, App
169	31.2	1.3	2655	2	US-08-463-483A-26	Sequence 17, Appl	242	30.6	1.3	2271	4	US-09-052-521C-3	Sequence 3, Appl
170	31.2	1.3	2655	2	US-08-471-046A-17	Sequence 17, Appl	243	30.6	1.3	2271	4	US-09-396-937-1	Sequence 1, Appl
171	31.2	1.3	2655	2	US-08-471-046A-26	Sequence 26, Appl	244	30.6	1.3	3698	4	US-09-976-594-1098	Sequence 1098, Ap
172	31.2	1.3	2655	2	US-08-471-046A-26	Sequence 17, Appl	245	30.6	1.3	8802	3	US-08-896-449A-1	Sequence 1, Appl
173	31.2	1.3	2655	2	US-08-470-566B-17	Sequence 17, Appl	246	30.6	1.3				

247	30.6	1.3	8802	3	US-09-132-652-1	Sequence 1, Appli	320	1.3	2409	4	US-09-252-991A-8479	Sequence 8479, Ap
248	30.6	1.3	10993	4	US-08-961-527-15	Sequence 15, Appl	321	1.3	3695	1	US-08-091-569-1	Sequence 1, Appli
249	30.6	1.3	1664976	4	US-08-916-421B-1	Sequence 1, Appli	322	1.3	3695	1	US-08-203-676-1	Sequence 1, Appli
C 250	30.4	1.3	393	3	US-09-252-991A-11602	Sequence 11602, A	323	1.3	3695	2	US-08-822-238-1	Sequence 1, Appli
C 251	30.4	1.3	437	3	US-08-714-918-52	Sequence 52, Appl	324	1.3	11459	4	US-09-462-136-7	Sequence 7, Appli
C 252	30.4	1.3	437	3	US-08-265-315-52	Sequence 52, Appl	325	1.3	19250	4	US-08-961-527-35	Sequence 35, Appl
C 253	30.4	1.3	437	3	US-09-265-315-52	Sequence 52, Appl	326	1.3	87563	4	US-09-453-702B-57	Sequence 57, Appl
C 254	30.4	1.3	437	3	US-09-266-417-52	Sequence 52, Appl	327	1.3	112132	4	US-09-741-150-3	Sequence 3, Appli
C 255	30.4	1.3	437	3	US-09-528-709-52	Sequence 52, Appl	328	1.3	112132	4	US-10-160-187-3	Sequence 3, Appli
C 256	30.4	1.3	437	3	US-09-527-745-52	Sequence 52, Appl	329	1.2	289	3	US-09-007-005-17	Sequence 17, Appl
C 257	30.4	1.3	447	3	US-08-933-983-20	Sequence 15639, A	330	1.2	289	3	US-09-244-796-17	Sequence 17, Appl
C 258	30.4	1.3	505	4	US-09-621-976-15639	Sequence 2733, Ap	331	1.2	423	3	US-09-040-984-61	Sequence 61, Appl
259	30.4	1.3	708	4	US-09-328-352-2733	Sequence 11775, A	332	1.2	423	4	US-09-123-912-61	Sequence 61, Appl
260	30.4	1.3	786	4	US-09-252-991A-11775	Sequence 13498, A	333	1.2	423	4	US-09-643-597-61	Sequence 61, Appl
261	30.4	1.3	819	4	US-09-252-991A-11775	Sequence 11662, A	334	1.2	423	4	US-09-480-884A-61	Sequence 61, Appl
C 262	30.4	1.3	1158	4	US-09-252-991A-11662	Sequence 3206, Ap	335	1.2	423	4	US-09-542-615A-61	Sequence 61, Appl
C 263	30.4	1.3	1257	4	US-09-543-681A-3206	Sequence 11775, A	336	1.2	423	4	US-09-606-421B-61	Sequence 61, Appl
264	30.4	1.3	1496	4	US-08-956-171E-274	Sequence 274, App	337	1.2	423	4	US-09-221-107-61	Sequence 61, Appl
265	30.4	1.3	1742	4	US-09-976-594-1127	Sequence 1127, Ap	338	1.2	484	4	US-09-621-976-35	Sequence 35, Appl
266	30.4	1.3	2351	4	US-09-620-312D-848	Sequence 848, App	339	1.2	576	4	US-09-540-236-402	Sequence 402, App
C 267	30.4	1.3	2940	3	US-09-195-868-11	Sequence 11, Appl	340	1.2	810	4	US-09-134-000C-2040	Sequence 2040, Ap
C 268	30.4	1.3	3204	4	US-09-252-991A-13955	Sequence 13955, A	341	1.2	922	4	US-09-621-976-1343	Sequence 1343, Ap
C 269	30.4	1.3	3691	3	US-09-195-868-12	Sequence 12, Appl	342	1.2	924	4	US-09-484-970B-42	Sequence 42, Appl
C 270	30.4	1.3	4147	3	US-08-560-005-1	Sequence 1, Appli	343	1.2	930	4	US-09-105-058C-17	Sequence 17, Appl
C 271	30.4	1.3	4147	3	US-09-418-540-1	Sequence 1, Appli	344	1.2	1001	4	US-09-641-638-162	Sequence 162, App
C 272	30.4	1.3	4147	3	US-09-969-528-1	Sequence 1, Appli	345	1.2	1522	3	US-09-413-574-1	Sequence 1, Appli
C 273	30.4	1.3	4870	3	US-08-664-962B-7	Sequence 7, Appli	346	1.2	1893	1	US-08-271-667B-5	Sequence 5, Appli
C 274	30.4	1.3	4870	3	US-09-311-743-7	Sequence 1, Appli	347	1.2	1893	3	US-08-765-889C-18	Sequence 18, Appl
C 275	30.4	1.3	640681	4	US-09-790-988-1	Sequence 1, Appli	348	1.2	1893	5	PCT-US95-07855-18	Sequence 18, Appl
276	30.2	1.3	624	4	US-09-134-000C-331	Sequence 331, App	349	1.2	2074	4	US-09-620-312D-258	Sequence 258, App
277	30.2	1.3	672	4	US-09-134-001C-1349	Sequence 1349, Ap	350	1.2	2101	3	US-08-765-889C-5	Sequence 5, Appli
278	30.2	1.3	687	4	US-09-252-991A-5646	Sequence 5646, Ap	351	1.2	2101	5	PCT-US95-07855-5	Sequence 5, Appli
C 279	30.2	1.3	702	4	US-09-252-991A-5549	Sequence 5549, Ap	352	1.2	2143	4	US-09-833-381-1022	Sequence 1022, Ap
280	30.2	1.3	868	4	US-09-071-035-71	Sequence 71, Appl	353	1.2	2304	1	US-08-271-667B-6	Sequence 6, Appli
281	30.2	1.3	906	4	US-09-134-000C-2609	Sequence 2609, Ap	354	1.2	2304	3	US-08-765-889C-19	Sequence 19, Appl
282	30.2	1.3	954	4	US-09-071-035-69	Sequence 69, Appl	355	1.2	2304	5	PCT-US95-07855-19	Sequence 19, Appl
C 283	30.2	1.3	1014	4	US-09-252-991A-10186	Sequence 10186, A	356	1.2	2563	4	US-09-016-434-1076	Sequence 1076, Ap
284	30.2	1.3	1068	4	US-09-107-532A-622	Sequence 622, App	357	1.2	2563	4	US-09-023-655-894	Sequence 894, App
C 285	30.2	1.3	1344	4	US-09-252-991A-7741	Sequence 7741, Ap	358	1.2	2565	4	US-09-105-058C-26	Sequence 26, Appl
286	30.2	1.3	1825	4	US-09-187-999-8	Sequence 8, Appli	359	1.2	2601	3	US-08-569-749-3	Sequence 3, Appli
C 287	30.2	1.3	1959	4	US-09-252-991A-7983	Sequence 7983, Ap	360	1.2	2601	5	PCT-US96-12860-3	Sequence 3, Appli
288	30.2	1.3	2010	4	US-09-252-991A-8169	Sequence 8169, Ap	361	1.2	2633	4	US-09-667-422-8	Sequence 8, Appli
289	30.2	1.3	2022	4	US-09-252-991A-9887	Sequence 9887, Ap	362	1.2	2880	4	US-09-235-451-1	Sequence 1, Appli
290	30.2	1.3	2316	4	US-09-252-991A-9887	Sequence 7830, Ap	363	1.2	2914	4	US-09-177-650-6	Sequence 6, Appli
291	30.2	1.3	16826	4	US-08-956-171E-46	Sequence 46, Appl	364	1.2	3721	4	US-09-620-312D-300	Sequence 300, App
C 292	30.2	1.3	50937	3	US-09-428-517-1	Sequence 1, Appli	365	1.2	7610	4	US-09-659-791A-12	Sequence 12, Appl
293	30	1.3	434	4	US-09-370-838-68	Sequence 68, Appl	366	1.2	314	3	US-09-328-111-35	Sequence 35, Appl
294	30	1.3	517	2	US-08-928-562-1	Sequence 1, Appli	367	1.2	417	4	US-09-540-236-573	Sequence 573, App
C 295	30	1.3	573	4	US-09-621-976-15325	Sequence 15325, A	368	1.2	426	4	US-09-494-921-4	Sequence 4, Appli
C 296	30	1.3	621	4	US-09-252-991A-15020	Sequence 15020, A	369	1.2	441	4	US-08-914-375C-54	Sequence 54, Appl
297	30	1.3	657	3	US-08-998-416-1061	Sequence 1061, Ap	370	1.2	441	4	US-08-914-375C-56	Sequence 56, Appl
298	30	1.3	681	4	US-09-252-991A-14735	Sequence 14735, A	371	1.2	441	4	US-09-621-976-9297	Sequence 9297, Ap
C 299	30	1.3	788	2	US-08-883-795A-35	Sequence 35, Appl	372	1.2	448	4	US-09-141-000-2	Sequence 2, Appli
C 300	30	1.3	823	2	US-08-785-750-1	Sequence 1, Appli	373	1.2	500	3	US-09-621-976-2506	Sequence 2506, Ap
C 301	30	1.3	823	4	US-09-205-337-1	Sequence 1, Appli	374	1.2	507	4	US-08-956-171E-797	Sequence 797, App
C 302	30	1.3	1002	4	US-09-543-681A-239	Sequence 239, App	375	1.2	544	4	US-09-641-638-517	Sequence 517, App
303	30	1.3	1170	4	US-09-489-039A-392	Sequence 392, App	376	1.2	1001	4	US-09-641-638-519	Sequence 519, App
304	30	1.3	1176	5	PCT-US95-15696-1	Sequence 1, Appli	377	1.2	1001	4	US-09-641-638-520	Sequence 520, App
305	30	1.3	1219	4	US-09-833-381-840	Sequence 840, App	378	1.2	1202	4	US-09-494-921-3	Sequence 3, Appli
C 306	30	1.3	1266	4	US-09-252-991A-14898	Sequence 14898, A	379	1.2	1319	4	US-09-594-506-43	Sequence 43, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 252, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 252
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22..576
; NAME/KEY: sig_peptide
; LOCATION: 22..69
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.4000009536743
; OTHER INFORMATION: seq ASVLLFLAWVCF/LFY
US-09-621-976-252

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Best Local Similarity 56.0%; Pred. No. 2.9e-06;
Matches 98; Conservative 1; Mismatches 76; Indels 0; Gaps 0;

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RESULT 2
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463

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RESULT 3
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

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RESULT 4
US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

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Db 237 GAGMKAWRASCMRRKRYAGSKTSYKSMWMTWRSWKYCYTKARWTGYCYRKGMMWGR 296
QY 1172 ATGTGCGGTCAATGAAAGATCCTGGGTTTGAGCAGTTTAAATGTGAGAAAGATTGC 1231
Db 297 GRWYASKYMKRWKWWCWAFMYRYSTGTRASMMWRRYTYTMMKWKYAWARAARWAM 356
QY 1232 ATGGGAACGTGATCAGACTGTACTTGGAGGA 1263
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RESULT 5
US-09-555-790A-1
; Sequence 1, Application US/09555790A
; Patent No. 655652
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo et al.
; TITLE OF INVENTION: TUMOR ANTIGEN PEPTIDE DERIVATIVES
; FILE REFERENCE: 0020-4716P
; CURRENT APPLICATION NUMBER: US/09/555,790A
; CURRENT FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(2438)
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; FEATURE:
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US-09-555-790A-1
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Best Local Similarity 55.9%; Pred. No. 0.68;
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QY 1666 GCCTCTG 1672
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RESULT 6
US-09-141-000-4/c
; Sequence 4, Application US/09141000
; Patent No. 6054295
; GENERAL INFORMATION:
; APPLICANT: Chen, Fang
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NUCLEAR
; TITLE OF INVENTION: RECEPTOR PROTEINS
; FILE REFERENCE: 1999Y
; CURRENT APPLICATION NUMBER: US/09/141,000
; CURRENT FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
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US-09-141-000-4
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Best Local Similarity 9.5%; Pred. No. 0.28;
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SUMMARIES

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32	2395	100.0	2395	8	ADA76569	Ada76569	Novel	hum
33	2395	100.0	2395	8	ABT44284	Abt44284	Human	PRO
34	2395	100.0	2395	8	ADB17196	Adb17196	Human	CDN
35	2395	100.0	2395	8	ACH03645	Ach03645	Human	sec
36	2395	100.0	2395	8	ADA20001	Ada20001	Novel	hum
37	2395	100.0	2395	8	ADB17384	Adb17384	Human	CDN
38	2395	100.0	2395	8	ADA20173	Ada20173	Novel	hum
39	2395	100.0	2395	8	ACD82159	Acd82159	Human	sec
40	2395	100.0	2395	8	ABT44567	Abt44567	Human	PRO
41	2395	100.0	2395	8	ACD82234	Acd82234	Human	sec
42	2395	100.0	2395	8	ADA00470	Ada00470	Human	sec
43	2395	100.0	2395	8	ACD42287	Acd42287	Human	CDN
44	2395	100.0	2395	8	ABT43940	Abt43940	Human	mem
45	2395	100.0	2395	8	ADB85712	Adb85712	Novel	hum
46	2395	100.0	2395	8	ADB83607	Adb83607	Novel	hum
47	2395	100.0	2395	8	ADB80713	Adb80713	Novel	hum
48	2395	100.0	2395	8	ADB73254	Adb73254	Novel	hum
49	2395	100.0	2395	8	ADB78336	Adb78336	Novel	hum
50	2395	100.0	2395	9	ADB84984	Adb84984	Human	PRO
51	2395	100.0	2395	9	ADB78090	Adb78090	Novel	hum
52	2395	100.0	2395	9	ADB87156	Adb87156	Human	PRO
53	2395	100.0	2395	9	ADB84738	Adb84738	Human	PRO
54	2395	100.0	2395	9	ADB68391	Adb68391	Human	PRO
55	2395	100.0	2395	9	ADB68198	Adb68198	Human	PRO
56	2395	100.0	2395	9	ADB83853	Adb83853	Novel	hum
57	2395	100.0	2395	9	ADB73008	Adb73008	Novel	hum
58	2395	100.0	2395	9	ADB91015	Adb91015	Novel	hum
59	2395	100.0	2395	9	AAD59353	Aad59353	Human	PRO
60	2395	100.0	2395	9	AAD59228	Aad59228	Human	PRO
61	2395	100.0	2395	9	ADC07095	Adc07095	Human	PRO
62	2395	100.0	2395	9	ADC17274	Adc17274	CDNA	sequ
63	2395	100.0	2395	9	ADC14972	Adc14972	Novel	hum
64	2395	100.0	2395	9	ADC36846	Adc36846	Human	PRO
65	2395	100.0	2395	9	ADC52467	Adc52467	Novel	hum
66	2395	100.0	2395	9	ADC21836	Adc21836	Human	PRO
67	2395	100.0	2395	9	ADC29800	Adc29800	Novel	hum
68	2395	100.0	2395	9	ADC49867	Adc49867	Novel	hum
69	2395	100.0	2395	9	ADC49066	Adc49066	Novel	hum
70	2395	100.0	2395	9	ADC49583	Adc49583	Novel	hum
71	2395	100.0	2395	9	ADC47444	Adc47444	Novel	hum
72	2395	100.0	2395	9	ADC47189	Adc47189	Novel	hum
73	2395	100.0	2395	9	ADC78064	Adc78064	Novel	hum
74	2395	100.0	2395	9	ADD06299	Add06299	Novel	hum
75	2395	100.0	2395	9	ADD10580	Add10580	Human	sec
76	2395	100.0	2395	9	ADC77818	Adc77818	Novel	hum
77	2395	100.0	2395	9	ADD11540	Add11540	Human	sec
78	2395	100.0	2395	9	ADD50781	Add50781	Novel	hum
79	2395	100.0	2395	9	ADD15377	Add15377	Novel	hum
80	2395	100.0	2395	9	ADD51027	Add51027	Novel	hum
81	2395	100.0	2395	9	ADD37333	Add37333	Human	sec
82	2395	100.0	2395	9	ADD36143	Add36143	Novel	hum
83	2395	100.0	2395	9	ADD50508	Add50508	Human	PRO
84	2395	100.0	2395	9	ADD50262	Add50262	Human	PRO
85	2395	100.0	2395	9	ADD51273	Add51273	Novel	hum
86	2395	100.0	2395	10	ADC48820	Adc48820	Novel	hum
87	2395	100.0	2395	10	ADC52277	Adc52277	Novel	hum
88	2395	100.0	2395	10	ADE20991	Ade20991	Novel	hum
89	2395	100.0	2395	10	ADE05835	Ade05835	Human	PRO
90	2395	100.0	2395	10	ADD75064	Add75064	Human	PRO
91	2395	100.0	2395	10	ADD75810	Add75810	Novel	hum
92	2395	100.0	2395	10	ADD85042	Add85042	Novel	hum
93	2395	100.0	2395	10	ADD86868	Add86868	Novel	hum
94	2395	100.0	2395	10	ADE20745	Ade20745	Novel	hum
95	2395	100.0	2395	10	ADE39042	Ade39042	Novel	hum
96	2395	100.0	2395	10	ADE05589	Ade05589	Human	PRO

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97	2395	100.0	2395	10	ADD73574	Human PRO	170	101.8	4.3	3671	7	ACA73517	Human sec
98	2395	100.0	2395	10	ADD78414	Novel hum	171	101.8	4.3	3671	7	ACA05832	Human sec
99	2395	100.0	2395	10	ADE41541	Human sec	172	101.8	4.3	3671	7	ACA66666	CDNA enco
100	2395	100.0	2395	10	ADE21237	Novel hum	173	101.8	4.3	3671	7	ACF20241	Human sec
101	2395	100.0	2395	10	ADD77352	Novel hum	174	101.8	4.3	3671	7	ACF19627	Human sec
102	2395	100.0	2395	10	ADE20499	Novel hum	175	101.8	4.3	3671	7	ACD21915	Human sec
103	2395	100.0	2395	10	ADD75564	Human PRO	176	101.8	4.3	3671	7	ACF13080	Human sec
104	2395	100.0	2395	10	ADD74080	Human PRO	177	101.8	4.3	3671	7	ACD25183	Human sec
105	2395	100.0	2395	10	ADD74326	Human PRO	178	101.8	4.3	3671	7	ACF00232	Human sec
106	2395	100.0	2395	10	ADD76056	Novel hum	179	101.8	4.3	3671	7	ACA72289	Novel hum
107	2395	100.0	2395	10	ADD85548	Novel hum	180	101.8	4.3	3671	7	ACD04813	Novel hum
108	2395	100.0	2395	10	ADE05097	Human PRO	181	101.8	4.3	3671	7	ACD18274	Human sec
109	2395	100.0	2395	10	ADD75310	Human PRO	182	101.8	4.3	3671	7	ACD08281	Human sec
110	2395	100.0	2395	10	ADD76854	Novel hum	183	101.8	4.3	3671	7	ACA88715	Novel hum
111	2395	100.0	2395	10	ADD86622	Novel hum	184	101.8	4.3	3671	7	ACA70157	Novel hum
112	2395	100.0	2395	10	ADD78090	Novel hum	185	101.8	4.3	3671	7	ACD12379	Novel hum
113	2395	100.0	2395	10	ADD77598	Novel hum	186	101.8	4.3	3671	7	ACC74294	Human sec
114	2395	100.0	2395	10	ADD77844	Novel hum	187	101.8	4.3	3671	7	ACD15922	Human sec
115	2395	100.0	2395	10	ADD85302	Novel hum	188	101.8	4.3	3671	7	ACD25490	Novel hum
116	2395	100.0	2395	10	ADD73834	Human PRO	189	101.8	4.3	3671	7	ACD17967	Human sec
117	2395	100.0	2395	10	ADD74572	Human PRO	190	101.8	4.3	3671	7	ACC88254	Human sec
118	2395	100.0	2395	10	ADD77100	Novel hum	191	101.8	4.3	3671	7	ACD21608	Human sec
119	2395	100.0	2395	10	ADD85794	Novel hum	192	101.8	4.3	3671	7	ACD18675	Human sec
120	2395	100.0	2395	10	ADE05343	Human PRO	193	101.8	4.3	3671	7	ABX98285	Human cDN
121	2395	100.0	2395	10	ADD74818	Human PRO	194	101.8	4.3	3671	7	ACD14036	Human PRO
122	1521.2	63.5	3197	4	AAK94266	Human ful	195	101.8	4.3	3671	7	ACD09816	Human sec
123	1417.6	59.2	2952	9	ADE07088	Novel cod	196	101.8	4.3	3671	7	ACC88561	Human sec
124	1266.6	52.9	3019	4	AAK94714	Human ful	197	101.8	4.3	3671	7	ACD21301	Human sec
125	1023.8	42.7	3310	9	ADE72573	Human end	198	101.8	4.3	3671	7	ABX75673	Human cDN
126	992.2	41.4	2755	6	ABN59875	Novel hum	199	101.8	4.3	3671	7	ABX97876	Human PRO
127	824	34.4	857	4	AAK93328	Human cDN	200	101.8	4.3	3671	7	ACA97352	Novel hum
128	808	33.7	816	9	ADE08866	Novel DNA	201	101.8	4.3	3671	7	ACA57815	Human PRO
129	731.6	30.5	818	4	AAK93603	Human cDN	202	101.8	4.3	3671	7	ACD14343	Human sec
130	731.6	30.5	818	4	AAK91771	Human cDN	203	101.8	4.3	3671	7	ACC91126	Human sec
131	510.4	21.3	566	4	AAK91872	Human cDN	204	101.8	4.3	3671	7	ACC88868	Human sec
132	510.4	21.3	566	4	ACH34160	Human end	205	101.8	4.3	3671	7	ACD07065	Human PRO
133	455.6	19.0	500	8	ABA12238	Human ner	206	101.8	4.3	3671	7	ACA67516	Human sec
134	411.4	17.2	451	5	AAH05366	Human cDN	207	101.8	4.3	3671	7	ACC81571	Human sec
135	277.4	11.6	801	4	AAH05366	Human cDN	208	101.8	4.3	3671	7	ACC89175	Human sec
136	277.4	11.6	1966	4	AAH14070	Human end	209	101.8	4.3	3671	7	ACC86531	Human sec
137	213.8	8.9	848	9	ADE72574	Human end	210	101.8	4.3	3671	7	ACC92968	Human sec
138	153	6.4	553	6	ABQ45840	Oligonuc	211	101.8	4.3	3671	7	ACA72596	Human PRO
139	153	6.4	553	6	ABQ45841	Oligonuc	212	101.8	4.3	3671	7	ACA89114	Human sec
140	146.2	6.1	553	6	ABQ45839	Oligonuc	213	101.8	4.3	3671	7	ACA89114	Human sec
141	146.2	6.1	553	6	ABQ45838	Oligonuc	214	101.8	4.3	3671	7	ACA69850	Human sec
142	101.8	4.3	1818	7	AAK95979	Human sec	215	101.8	4.3	3671	7	ACA96993	Novel hum
143	101.8	4.3	2559	7	AAK95978	Human sec	216	101.8	4.3	3671	7	ACA90989	Novel hum
144	101.8	4.3	2717	8	AAK95978	Human sec	217	101.8	4.3	3671	7	ACA70771	Human sec
145	101.8	4.3	2744	4	AAH98909	Human EST	218	101.8	4.3	3671	7	ACA95281	Novel hum
146	101.8	4.3	2744	4	AAH98909	Human EST	219	101.8	4.3	3671	7	ACC86224	Human sec
147	101.8	4.3	3671	4	AAAF37051	Human PRO	220	101.8	4.3	3671	7	ACC90096	Human sec
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153	101.8	4.3	3671	4	AAAF37051	DNA enco	226	101.8	4.3	3671	7	ACA74597	CDNA enco
154	101.8	4.3	3671	4	AAAF37051	DNA enco	227	101.8	4.3	3671	7	ACA74597	CDNA enco
155	101.8	4.3	3671	4	AAAF37051	DNA enco	228	101.8	4.3	3671	7	ACA70464	Human sec
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157	101.8	4.3	3671	4	AAAF37051	DNA enco	230	101.8	4.3	3671	7	ACA68322	Novel hum
158	101.8	4.3	3671	4	AAAF37051	DNA enco	231	101.8	4.3	3671	7	ABX98787	Novel hum
159	101.8	4.3	3671	4	AAAF37051	DNA enco	232	101.8	4.3	3671	7	ACC81264	Human sec
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161	101.8	4.3	3671	4	AAAF37051	DNA enco	234	101.8	4.3	3671	7	ACD04506	Novel hum
162	101.8	4.3	3671	4	AAAF37051	DNA enco	235	101.8	4.3	3671	7	ACC87947	Human sec
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164	101.8	4.3	3671	4	AAAF37051	DNA enco	237	101.8	4.3	3671	7	ACA96324	Human PRO
165	101.8	4.3	3671	4	AAAF37051	DNA enco	238	101.8	4.3	3671	7	ACA65098	Human PRO
166	101.8	4.3	3671	4	AAAF37051	DNA enco	239	101.8	4.3	3671	7	ACA73824	Human sec
167	101.8	4.3	3671	4	AAAF37051	DNA enco	240	101.8	4.3	3671	7	ACA74236	Novel hum
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369 101.8 4.3 3671 8 ACF60183 Acf60183 Human sec
370 101.8 4.3 3671 8 ACF46733 Acf46733 Human sec
371 101.8 4.3 3671 8 ACF75590 Acf75590 Human sec
372 101.8 4.3 3671 8 ADA79809 Ada79809 Human sec
373 101.8 4.3 3671 8 ACF17250 Acf17250 Human sec
374 101.8 4.3 3671 8 ACF23004 Acf23004 Human sec
375 101.8 4.3 3671 8 ACF08004 Acf08004 Human sec
376 101.8 4.3 3671 8 ACF08311 Acf08311 Human sec
377 101.8 4.3 3671 8 ACF40615 Acf40615 Human sec
378 101.8 4.3 3671 8 ACF53794 Acf53794 Human sec
379 101.8 4.3 3671 8 ACD47058 Acd47058 Human sec
380 101.8 4.3 3671 8 ACF47961 Acf47961 Human sec
381 101.8 4.3 3671 8 ACF47347 Acf47347 Human sec
382 101.8 4.3 3671 8 ACF46119 Acf46119 Human sec
383 101.8 4.3 3671 8 ACD86208 Acd86208 Human sec
384 101.8 4.3 3671 8 ACF52566 Acf52566 Human sec
385 101.8 4.3 3671 8 ACF52873 Acf52873 Human sec
386 101.8 4.3 3671 8 ACF64866 Acf64866 Human sec
387 101.8 4.3 3671 8 ACF76511 Acf76511 Human sec
388 101.8 4.3 3671 8 ACF76511 Acf76511 Human sec

XX 01-MAR-2000; 2000WO-US005601.
PF 23-MAR-1999; 99US-0125774P.
XX 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0131291P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132383P.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 09-DEC-1999; 99US-0170262P.
XX
PA (GETH) GENENTECH INC.
XX
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2000-628263/60.
DR P-PSDB; AAB18918.
XX
PT Novel secreted and transmembrane polypeptides useful for diagnosing tumor
PT in a mammal, for identifying agonists and antagonists of the polypeptide
PT and for therapeutic use.
XX
PS Claim 2; Fig 19; 222pp; English.
XX
CC The present sequence encodes a secreted or transmembrane polypeptide. The
CC specification describes polypeptides designated PRO1484, PRO4334,
CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
CC useful for diagnosing tumour in a mammal. The polypeptides, their
CC agonists and antagonists are useful treating a condition associated with
CC expression or activity of the polypeptide. Conditions treated include
CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are
CC capable of inducing proliferation of mammalian kidney mesangial cells and
CC are therefore useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Bergers disease or other
CC nephropathies associated with Schonlein-Henoch purpura, celiac disease,
CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
CC to generate transgenic animals for use in development and screening of
CC therapeutically useful reagents and also for chromosome identification
CC and tissue typing
XX
SQ Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;

Query Match 100.0%; Score 2395; DB 3; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGAGCCGGAAGCGCGCTGCAGAGGGCGAGGCTCCAGTGGGGTCCGTTCCGCATC 60
Db |||||
1 CCTGGAGCCGGAAGCGCGCTGCAGAGGGCGAGGCTCCAGTGGGGTCCGTTCCGCATC 60
QY 61 CAGCCTAGCGTGTCACAGATCGCGTGGGCTCCGGGATCTTCGTTACCTGTTGCGTAGCG 120
Db |||||
61 CAGCCTAGCGTGTCACAGATCGCGTGGGCTCCGGGATCTTCGTTACCTGTTGCGTAGCG 120
QY 121 ATCGAGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATCTTCGGGCTCCCGTTCGTTCC 180
Db |||||
121 ATCGAGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATCTTCGGGCTCCCGTTCGTTCC 180
QY 181 TCTGCCAGAGCGGAACACGGAGCGGAGCCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
Db |||||

Db 181 TCTGCCAGAGCGGAACACGGAGCGGAGCCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
QY 241 TCTAACTGGACCACCGCTGCCACCACTCTCTTTCAGTAAAGTTGTTATTTCTGTATAGAT 300
Db |||||
241 TCTAACTGGACCACCGCTGCCACCACTCTCTTTCAGTAAAGTTGTTATTTCTGTATAGAT 300
QY 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGGTGTGAATTTATGCCCTACACAAC 360
Db |||||
301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGGTGTGAATTTATGCCCTACACAAC 360
QY 361 TACCTTGTGAAAAAGGAGCATCTCACAGTTTGTGGTGAAGCAAAAGCCACCTACAGTT 420
Db |||||
361 TACCTTGTGAAAAAGGAGCATCTCACAGTTTGTGGTGAAGCAAAAGCCACCTACAGTT 420
QY 421 ACTATGCCTCGAATCAAGGCATGTGATGACGGGAGCCTTCCTGGCTTGTGACGTCATC 480
Db |||||
421 ACTATGCCTCGAATCAAGGCATGTGATGACGGGAGCCTTCCTGGCTTGTGACGTCATC 480
QY 481 AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCT 540
Db |||||
481 AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCT 540
QY 541 GGA AAAAGAAATAGTCTTTTATGGAGATGAAACCTGGGTAAATATTCCCAAAGCATT 600
Db |||||
541 GGA AAAAGAAATAGTCTTTTATGGAGATGAAACCTGGGTAAATATTCCCAAAGCATT 600
QY 601 GTGGAATATGATGGAACAACCTCATTTTTCGTGTGATTAACAGAGGTGGATAAATAAT 660
Db |||||
601 GTGGAATATGATGGAACAACCTCATTTTTCGTGTGATTAACAGAGGTGGATAAATAAT 660
QY 661 GTCACGAGGCATTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAAATCCTCCAC 720
Db |||||
661 GTCACGAGGCATTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAAATCCTCCAC 720
QY 721 TACCTGGGGCTGGACCACATTTGGCCACATTTTTCAGGGCCCCAACAGCCCCCTGATTGGG 780
Db |||||
721 TACCTGGGGCTGGACCACATTTGGCCACATTTTTCAGGGCCCCAACAGCCCCCTGATTGGG 780
QY 781 AAGCTGAGCGAGATGGACAGCGTCTGTGATGAAGATCCACACCTCACTGAGTGAAGGAG 840
Db |||||
781 AAGCTGAGCGAGATGGACAGCGTCTGTGATGAAGATCCACACCTCACTGAGTGAAGGAG 840
QY 841 AGAGAGACGCTTTTACCCAAATTTGCTGTTCTTTTGTGGTGACCATGGCATGTCTGAAACA 900
Db |||||
841 AGAGAGACGCTTTTACCCAAATTTGCTGTTCTTTTGTGGTGACCATGGCATGTCTGAAACA 900
QY 901 GGAAGTCACGGGGCTCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCT 960
Db |||||
901 GGAAGTCACGGGGCTCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCT 960
QY 961 GCGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGCACGTCCTCAATAGACGGATGTG 1020
Db |||||
961 GCGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGCACGTCCTCAATAGACGGATGTG 1020
QY 1021 GCTGCGACACTGGCGATAGCATTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC 1080
Db |||||
1021 GCTGCGACACTGGCGATAGCATTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC 1080
QY 1081 CTATTCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
Db |||||
1081 CTATTCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
QY 1141 ACAGTGCAGCTTAGTAAACCTGTTGCAAGAGAATGTGCCGTATATGAAAAAGATCCTGGG 1200
Db |||||
1141 ACAGTGCAGCTTAGTAAACCTGTTGCAAGAGAATGTGCCGTATATGAAAAAGATCCTGGG 1200
QY 1201 TTTGAGCAGTTTAAATGTCAGAAAGATTGCGTGGGATTCGATGGGAATGAGTGTGAG 1260
Db |||||
1201 TTTGAGCAGTTTAAATGTCAGAAAGATTGCGTGGGATTCGATGGGAATGAGTGTGAG 1260
QY 1261 GAAAAAGCATTTCAGAGTCTTATTAACCTGGGCTCAAGGTTCTCAGGAGTCTGAT 1320
Db |||||
1261 GAAAAAGCATTTCAGAGTCTTATTAACCTGGGCTCAAGGTTCTCAGGAGTCTGAT 1320

QY	1321	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGACAAGTGGCCCGAGTTCTTCACCTGCTCC	1380
Db	1321		
QY	1381	TGCTCAGCGTCCCACAGGCACTGCACAGAAAGCTGAGCTGGAAGTCCCACTGTCTATCTC	1440
Db	1381		
QY	1441	CTGGGTTTCTCTGCTCTTTTAATTGGTGATCCTGGTTCTTTCGGCCGTTTCACGTCATTG	1500
Db	1441		
QY	1501	TGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGCAGGCT	1560
Db	1501		
QY	1561	GCCTTTCGTTTACAGACTCTGTTTGAAACACCTGGTGTGTGCCAAGTCTGGCAGTGCCC	1620
Db	1561		
QY	1621	TGGACAGGGGCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCTCC	1680
Db	1621		
QY	1681	GACACAGGTGTTACATCTGTGCTCAGGTCAGATGCCCTCAGTCTTGGAAAGCTAGGT	1740
Db	1681		
QY	1741	TCCTGCGACTGTTACCAAGTGATTGTTAAAGAGCTGGCGGTACACAGAGGAACAAGCCCC	1800
Db	1741		
QY	1801	CAGCTGAGGGGTGTGTGAATCGGACAGCCTCCAGCAGAGGTGTGGAGCTGCAGCTGA	1860
Db	1801		
QY	1861	GGGAAGAAGAGACAATCGGCCCTGGACACTCAGAGGGTCAAAGGAGACTTGGTCGCACC	1920
Db	1861		
QY	1921	ACTCATCTGCCACCCCGAATGCATCCTGCCCTCATCAGGTCAGATTTCTTTCCAAGG	1980
Db	1921		
QY	1981	CGGACGTTTCTGTTGGAAATCTTAGTCTTGGCCTCGGACACCTTCATTGTTAGCTGG	2040
Db	1981		
QY	2041	GGAGTGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCCA	2100
Db	2041		
QY	2101	GGATCAAGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCCCAACCTGCAC	2160
Db	2101		
QY	2161	AGCCCTCATCCCTCTTGGCTTGAGCCGTGAGGGCCCTGTGCTGAGTGTCTGACCGAGA	2220
Db	2161		
QY	2221	CACTCACAGCTTTGTTCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTGCCACG	2280
Db	2221		
QY	2281	CTTGCACTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG	2340
Db	2281		
QY	2341	CTGCACACAGTATGTAGTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA	2395
Db	2341		

RESULT 2	
AAD02923	
ID	AAD02923 standard; cDNA; 2395 BP.
XX	
AC	AAD02923;
XX	
DT	31-MAY-2001 (first entry)
XX	
DE	Human PRO4405 cDNA (DNA84920-2614).
XX	
KW	Human; PRO4405; antiinflammatory; dermatological; immunosuppressive;
KW	antirheumatic; antiarthritic; osteopathic; antianaemic; haemostatic;
KW	antithyroid; antidiabetic; antiviral; antipsoriatic; antiallergic;
KW	antisthmatic; inhibitor; therapy; systemic lupus erythematosus;
KW	spondyloarthropathy; systemic sclerosis; systemic vasculitis;
KW	sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome;
KW	autoimmune thrombocytopenia; immune-mediated renal disease; hepatitis;
KW	demyelinating polyneuropathy; Guillian-Barre syndrome; Whipple's disease;
KW	hepatobiliary disease; primary biliary cirrhosis; sclerosing cholangitis;
KW	inflammatory bowel disease; gluten-sensitive enteropathy; skin disease;
KW	allergic rhinitis; atopic dermatitis; food hypersensitivity; urticaria;
KW	eosinophilic pneumonia; hypersensitivity pneumonitis; graft rejection;
KW	idiopathic pulmonary fibrosis; graft-versus-host-disease; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	79..1011
FT	/*tag= a
FT	/product= "Human PRO4405 protein"
FT	sig_peptide
FT	79..180
FT	/*tag= b
FT	mat_peptide
FT	181..1008
FT	/*tag= c
FT	/product= "Mature human PRO4405 protein"
XX	
PN	WO200116319-A2.
XX	
PD	08-MAR-2001.
XX	
PF	23-AUG-2000; 2000WO-US023522.
XX	
PR	31-AUG-1999; 99US-0151733P.
PR	01-SEP-1999; 99WO-US020111.
PR	16-DEC-1999; 99WO-US030095.
PR	18-FEB-2000; 2000WO-US004342.
PR	01-MAR-2000; 2000WO-US005601.
PR	30-MAR-2000; 2000WO-US008439.
PR	17-MAY-2000; 2000WO-US013705.
PR	22-MAY-2000; 2000WO-US014042.
PR	30-MAY-2000; 2000WO-US014941.
PR	05-JUN-2000; 2000US-0209832P.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Tumas D;
PI	Watanabe CK, Wood WI;
XX	
DR	WPI; 2001-226690/23.
DR	P-PSDB; AAY72877.
XX	
PT	New PRO polypeptides for treating immune related and inflammatory
PT	diseases such as rheumatoid arthritis, systemic vasculitis, asthma,
PT	autoimmune hemolytic anemia, and diabetes mellitus.
XX	
PS	Claim 2; Fig 7; 118pp; English.
XX	
CC	The present sequence is a cDNA (DNA84920-2614 clone) encoding PRO4405
CC	protein. PRO protein, its agonist or antagonist or its antibody which are
CC	capable of enhancing or inhibiting the proliferation of T-lymphocytes or
CC	of increasing the infiltration of inflammatory cells into a tissue are
CC	useful in the diagnosis and treatment of immune-related diseases in

CC mammals. The PRO protein is useful for treating systemic lupus
CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
CC arthritis, spondyloarthropathy, systemic sclerosis, idiopathic
CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia,
CC thyroiditis, diabetes mellitus, immune-mediated renal disease,
CC demyelinating disease of the central or peripheral nervous system,
CC idiopathic demyelinating polyneuropathy, Guillian-Barre syndrome, chronic
CC inflammatory demyelinating polyneuropathy, hepatobiliary disease,
CC infectious or autoimmune chronic active hepatitis, primary biliary
CC cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory
CC bowel disease, gluten-sensitive enteropathy, Whipple's disease,
CC autoimmune or immune-mediated skin diseases such as bullous skin diseases,
CC erythema multiforme and contact dermatitis, psoriasis, allergic diseases
CC such as asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity and urticaria, immunologic diseases of the lung such as
CC eosinophilic pneumonias, idiopathic pulmonary fibrosis, hyper-
CC sensitivity pneumonitis, transplantation associated diseases such as
CC graft rejection or graft-versus-host-disease
XX
SQ Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;

Query Match 100.0%; Score 2395; DB 4; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CCTGGAGCCGGAAGCGCGCTGCAGCAGGCGGAGGCTCCAGGTGGGTTCGGTCCGCATC	60
Db	1	CCTGGAGCCGGAAGCGCGCTGCAGCAGGCGGAGGCTCCAGGTGGGTTCGGTCCGCATC	60
QY	61	CAGCCTAGCGTGTCCACGATCGGCTCGGCTCCGAGCTTTCGCTACCTGTTCGATAGC	120
Db	61	CAGCCTAGCGTGTCCACGATCGGCTCGGCTCCGAGCTTTCGCTACCTGTTCGATAGC	120
QY	121	ATCGAGGTGCTAGGATCGCGTCTTCCTTCGGGATTCCTCCGGCTCCCGTTCGTTCC	180
Db	121	ATCGAGGTGCTAGGATCGCGTCTTCCTTCGGGATTCCTCCGGCTCCCGTTCGTTCC	180
QY	181	TCTGCCAGAGCGGAACACGAGCGGAGCCCGCCAGCGCCGAAACCTCGGTGGAGCCAGT	240
Db	181	TCTGCCAGAGCGGAACACGAGCGGAGCCCGCCAGCGCCGAAACCTCGGTGGAGCCAGT	240
QY	241	TCTAACTGGACACGCTGCCACCCTCTCTTCAGTAAAGTTGTTATGTTCTGATAGAT	300
Db	241	TCTAACTGGACACGCTGCCACCCTCTCTTCAGTAAAGTTGTTATGTTCTGATAGAT	300
QY	301	GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGTTGTAATTTATGCCCTACACAAC	360
Db	301	GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGTTGTAATTTATGCCCTACACAAC	360
QY	361	TACCTTGAGAGATGATTTTGTGTTGGGTCAAAGGTTGTAATTTATGCCCTACACAAC	420
Db	361	TACCTTGAGAGATGATTTTGTGTTGGGTCAAAGGTTGTAATTTATGCCCTACACAAC	420
QY	421	ACTATGCCTCGAATCAAGGCATTCACAGTTCGAGCGGAGCCTTCCTGGCTTTCGACGTCATC	480
Db	421	ACTATGCCTCGAATCAAGGCATTCACAGTTCGAGCGGAGCCTTCCTGGCTTTCGACGTCATC	480
QY	481	AGGAACCTCAATTCTCCTGCACCTGCTGGAACACAGTGTGATAAGACAAAGCAGCT	540
Db	481	AGGAACCTCAATTCTCCTGCACCTGCTGGAACACAGTGTGATAAGACAAAGCAGCT	540
QY	541	GGAAAAAGATAGTCTTTTATGGAGATGAACCTGGGTTAAATTTATCCAAAGCATTTT	600
Db	541	GGAAAAAGATAGTCTTTTATGGAGATGAACCTGGGTTAAATTTATCCAAAGCATTTT	600
QY	601	GTGGAATATGATGGAAACAACTCATTTTTCGTTGATACACAGAGGTGATAATAAT	660
Db	601	GTGGAATATGATGGAAACAACTCATTTTTCGTTGATACACAGAGGTGATAATAAT	660
QY	661	GTCACGAGGCATTTGGATAAAGTATTAAGAGAGGAGATTGGGACATATTAATCCTCCAC	720
Db	661	GTCACGAGGCATTTGGATAAAGTATTAAGAGAGGAGATTGGGACATATTAATCCTCCAC	720

QY	721	TACCTGGGGCTGGACCAACATTTGGCCACATTTTACGGGCCCCAACAGCCCCCTGATTGGGAG	780
Db	721	TACCTGGGGCTGGACCAACATTTGGCCACATTTTACGGGCCCCAACAGCCCCCTGATTGGGAG	780
QY	781	AAGCTGAGCGAGATGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGAG	840
Db	781	AAGCTGAGCGAGATGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGAG	840
QY	841	AGAGAGACGCTTTTACCAATTTGCTGGTCTTTTGGTGGTGAATACACCTCTGATTTTAATCAGTTCT	900
Db	841	AGAGAGACGCTTTTACCAATTTGCTGGTCTTTTGGTGGTGAATACACCTCTGATTTTAATCAGTTCT	900
QY	901	GGAAGTCACGGGGCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT	960
Db	901	GGAAGTCACGGGGCTCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT	960
QY	961	GCGTTTGAAGGAAACCCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTG	1020
Db	961	GCGTTTGAAGGAAACCCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTG	1020
QY	1021	GCTGCGACACTGGCGATAGCACTTGGCTTACGATTTCCAAAGACAGTGTAGGAGCCTC	1080
Db	1021	GCTGCGACACTGGCGATAGCACTTGGCTTACGATTTCCAAAGACAGTGTAGGAGCCTC	1080
QY	1081	CTATTTCCAGTTTGTGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT	1140
Db	1081	CTATTTCCAGTTTGTGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT	1140
QY	1141	ACAGTGCAGCTTAGTAAACTGTTGCAAGAGATGTGCCGTATATGAAAAAGATCTCTGGG	1200
Db	1141	ACAGTGCAGCTTAGTAAACTGTTGCAAGAGATGTGCCGTATATGAAAAAGATCTCTGGG	1200
QY	1201	TTTGAGCAGTTTAAATGTCAGAAAGATTGATGGGAACTGGATCAGACTGATCTTGGAG	1260
Db	1201	TTTGAGCAGTTTAAATGTCAGAAAGATTGATGGGAACTGGATCAGACTGATCTTGGAG	1260
QY	1261	GAAAAGCATTCAGAACTCTTCAACCTGGGCTCAAAGTTCTCAGGCACTGATCTGGAT	1320
Db	1261	GAAAAGCATTCAGAACTCTTCAACCTGGGCTCAAAGTTCTCAGGCACTGATCTGGAT	1320
QY	1321	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCAAGTGCCCAAGTTCTCACCTGCTCC	1380
Db	1321	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCAAGTGCCCAAGTTCTCACCTGCTCC	1380
QY	1381	TGCTCAGCGTCCACAGGCACTGCAAGAAAGCTGAGCTGGAAGTCCCACTGTCTATCTC	1440
Db	1381	TGCTCAGCGTCCACAGGCACTGCAAGAAAGCTGAGCTGGAAGTCCCACTGTCTATCTC	1440
QY	1441	CTGGGTTTCTCTGCTCTTTTATTTGTTGATCTGTTCTTTCGGCCCTTCTCAGCTCATTTG	1500
Db	1441	CTGGGTTTCTCTGCTCTTTTATTTGTTGATCTGTTCTTTCGGCCCTTCTCAGCTCATTTG	1500
QY	1501	TGTGCACCTCAGCTGAAAGTTCTGTTGCTTCTTGTGGCTCTCTGTTGGCTGGCGGAGCT	1560
Db	1501	TGTGCACCTCAGCTGAAAGTTCTGTTGCTTCTTGTGGCTCTCTGTTGGCTGGCGGAGCT	1560
QY	1561	GCCTTTCTGTTTACCACTCTGTTGTAACACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1620
Db	1561	GCCTTTCTGTTTACCACTCTGTTGTAACACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1620
QY	1621	TGGACAGGGGGCTCAGGGAAGGACGTGGAGCAGCTTATCCAGGCTCTGGGTGTTCC	1680
Db	1621	TGGACAGGGGGCTCAGGGAAGGACGTGGAGCAGCTTATCCAGGCTCTGGGTGTTCC	1680
QY	1681	GACACAGGTGTTTACATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1740
Db	1681	GACACAGGTGTTTACATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1740
QY	1741	TCCTGGACTGTTTACCAAGGTGTTTAAAGAGCTGGCGGTTCAGAGGAACAAGCCCC	1800
Db	1741	TCCTGGACTGTTTACCAAGGTGTTTAAAGAGCTGGCGGTTCAGAGGAACAAGCCCC	1800

QY 1801 CAGCTGAGGGGGTGTGTAATCGGACAGCCTCCACAGAGAGGTGTGGAGCTGCAGCTGA 1860
Db 1801 CAGCTGAGGGGGTGTGTAATCGGACAGCCTCCACAGAGAGGTGTGGAGCTGCAGCTGA 1860
QY 1861 GGGGAAGAAGAGACAATCGCCTGGACACTCAGGAGGGTCAAAAGGAGACTTGGTCCGACC 1920
Db 1861 GGGGAAGAAGAGACAATCGCCTGGACACTCAGGAGGGTCAAAAGGAGACTTGGTCCGACC 1920
QY 1921 ACTCATCCTGCCACCCAGAAATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCAAGG 1980
Db 1921 ACTCATCCTGCCACCCAGAAATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCAAGG 1980
QY 1981 CGGACGTTTCTGTTGGAATTTCTAGTCTTGGCCTCGGACACCTTCATTCGTTAGCTGG 2040
Db 1981 CGGACGTTTCTGTTGGAATTTCTAGTCTTGGCCTCGGACACCTTCATTCGTTAGCTGG 2040
QY 2041 GGAGTGGTGGTGAAGCAGTGAAGAAGAGCGGATGGTCCACTCAGATCCACAGAGCCCA 2100
Db 2041 GGAGTGGTGGTGAAGCAGTGAAGAAGAGCGGATGGTCCACTCAGATCCACAGAGCCCA 2100
QY 2101 GGATCAAGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCACCCCTGCAC 2160
Db 2101 GGATCAAGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCACCCCTGCAC 2160
QY 2161 AGCCCTCATCCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGTCTGACCGAGA 2220
Db 2161 AGCCCTCATCCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGTCTGACCGAGA 2220
QY 2221 CACTCAGCTTGTGCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTGCCACG 2280
Db 2221 CACTCAGCTTGTGCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTGCCACG 2280
QY 2281 CTTGCACCTCGGCCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG 2340
Db 2281 CTTGCACCTCGGCCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG 2340
QY 2341 CTGCACACAGTATGTAGTTACCAAAAGAAATAAACCAGCAATAATTGAGAAAAAAA 2395
Db 2341 CTGCACACAGTATGTAGTTACCAAAAGAAATAAACCAGCAATAATTGAGAAAAAAA 2395

RESULT 3
AAF92127
ID AAF92127 standard; cDNA; 2395 BP.

XX AAF92127;
AC 15-MAY-2001 (first entry)
DT Human PRO4405 cDNA.
XX Human; PRO protein; mapping; ss.
OS Homo sapiens.
XX WO200116318-A2.
XX 08-MAR-2001.
XX 24-AUG-2000; 2000WO-US023328.
XX 01-SEP-1999; 99WO-US020111.
XX 15-SEP-1999; 99WO-US021090.
XX 07-DEC-1999; 99US-0169495P.
XX 09-DEC-1999; 99US-0170262P.
XX 11-JAN-2000; 2000US-0175481P.
XX 18-FEB-2000; 2000WO-US004341.
XX 22-FEB-2000; 2000WO-US004414.
XX 01-MAR-2000; 2000WO-US005601.
XX 03-MAR-2000; 2000US-0187202P.
XX 21-MAR-2000; 2000US-0191007P.
XX 30-MAR-2000; 2000WO-US008439.

PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX (GETH) GENENTECH INC.
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2001-183260/18.
DR P-PSDB; AAB87595.
XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX Claim 2; Fig 139; 278pp; English.
PS The present sequence is the coding sequence for a human PRO polypeptide
XX (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC antagonists or anti-PRO antibodies are useful for preparation of a
CC medicament useful in the treatment of a condition which is responsive to
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping
XX Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 2395; DB 4; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGAGCCGGAAGCGCGGCTGCAGCAGCGCGAGGCTCCAGGTGGGTCCGCATC 60
Db 1 CCTGGAGCCGGAAGCGCGGCTGCAGCAGCGCGAGGCTCCAGGTGGGTCCGCATC 60
QY 61 CAGCCTAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTTCGTACCTGTTCGTAGCG 120
Db 61 CAGCCTAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTTCGTACCTGTTCGTAGCG 120
QY 121 ATCGAGGTGTAGGATCGCGGTCTTCTTCGGGGATTTCTCCCGGCTCCCGTTCGTTCC 180
Db 121 ATCGAGGTGTAGGATCGCGGTCTTCTTCGGGGATTTCTCCCGGCTCCCGTTCGTTCC 180
QY 181 TCTGCCAGAGCGGAACACGGAGCGGAGCCCGCCGAGCCCGCCGAGCCAGT 240
Db 181 TCTGCCAGAGCGGAACACGGAGCGGAGCCCGCCGAGCCCGCCGAGCCAGT 240
QY 241 TCTAACTGGACCAAGCTGCCACCCTCTCTTCAGTAAAGTTGTTATTCTGTATAGAT 300
Db 241 TCTAACTGGACCAAGCTGCCACCCTCTCTTCAGTAAAGTTGTTATTCTGTATAGAT 300
QY 301 GCCTTGAGAGATGATTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACT 360
Db 301 GCCTTGAGAGATGATTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACT 360
QY 361 TACCTTGAGAGATGATTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACAGTT 420
Db 361 TACCTTGAGAGATGATTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACAGTT 420
QY 421 ACTATGCCTCGAATCAAGGCATTTGATGACGGGGAGGCTTCTCGGCTTCGACGTCATC 480
Db 421 ACTATGCCTCGAATCAAGGCATTTGATGACGGGGAGGCTTCTCGGCTTCGACGTCATC 480
QY 481 AGGAACCTCAATTTCTCTGCACACTGCTGGAAGACAGTGTGATAAGACAAAGCAGCT 540
Db 481 AGGAACCTCAATTTCTCTGCACACTGCTGGAAGACAGTGTGATAAGACAAAGCAGCT 540
QY 541 GGAAAAAAGAATAGTCTTTTATGGAGATGAAACCTGGGTAAATTTATCCCAAAGCATTTT 600
Db 541 GGAAAAAAGAATAGTCTTTTATGGAGATGAAACCTGGGTAAATTTATCCCAAAGCATTTT 600

Db 1021 GCTGCGACACTGGCGATAGCACCTTGGCTTACCGATTCCAAAAGACAGTGTAGGAGCCTC 1080
QY 1081 CTATTCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
Db 1081 CTATTCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
QY 1141 ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCCGTCAATGAAAAAGATCCTGGG 1200
Db 1141 ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCCGTCAATGAAAAAGATCCTGGG 1200
QY 1201 TTTGAGCAGTTTAAATGTCAGAAAGATTGCATGGAACTGGATCAGACTGTACTTTGGAG 1260
Db 1201 TTTGAGCAGTTTAAATGTCAGAAAGATTGCATGGAACTGGATCAGACTGTACTTTGGAG 1260
QY 1261 GAAAAGCATTCAGAAAGTCCTATTCAACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT 1320
Db 1261 GAAAAGCATTCAGAAAGTCCTATTCAACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT 1320
QY 1321 GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCAGTTCTCACCCCTGCTCC 1380
Db 1321 GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCAGTTCTCACCCCTGCTCC 1380
QY 1381 TGCTCAGCGTCCACAGGCACCTGCACAGAAAGGCTGAGCTGGAAGTCCCACCTGTCACTC 1440
Db 1381 TGCTCAGCGTCCACAGGCACCTGCACAGAAAGGCTGAGCTGGAAGTCCCACCTGTCACTC 1440
QY 1441 CTGGGTTTCTCTGTCTCTTTTATTGGTGATCCTGGTTCTTTGCGCCGTTACGTCATTG 1500
Db 1441 CTGGGTTTCTCTGTCTCTTTTATTGGTGATCCTGGTTCTTTGCGCCGTTACGTCATTG 1500
QY 1501 TGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCCCTCTCGTGGCTGGCGGAGGCT 1560
Db 1501 TGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCCCTCTCGTGGCTGGCGGAGGCT 1560
QY 1561 GCCTTTTCGTTTACCAGACTCTGGTTGAAACACCTGGTGTGTCGCAAGTGTGGCAGTGCCC 1620
Db 1561 GCCTTTTCGTTTACCAGACTCTGGTTGAAACACCTGGTGTGTCGCAAGTGTGGCAGTGCCC 1620
QY 1621 TGGACAGGGGGCCTCAGGGAAAGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCC 1680
Db 1621 TGGACAGGGGGCCTCAGGGAAAGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCC 1680
QY 1681 GACACAGGTGTTACATCTGTGCTGTGTCAGGTGAGTGCCTCAGTTCTTGGAAAGCTAGGT 1740
Db 1681 GACACAGGTGTTACATCTGTGCTGTGTCAGGTGAGTGCCTCAGTTCTTGGAAAGCTAGGT 1740
QY 1741 TCCTGCGACTGTTACCAAGTGATTGTAAGAGCTGCGGTTCACAGAGGAACAAGCCCCC 1800
Db 1741 TCCTGCGACTGTTACCAAGTGATTGTAAGAGCTGCGGTTCACAGAGGAACAAGCCCCC 1800
QY 1801 CAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCACAGAGAGGTGTGGAGCTGCAGCTGA 1860
Db 1801 CAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCACAGAGAGGTGTGGAGCTGCAGCTGA 1860
QY 1861 GGGAAAGAGAGACAATCGGCCCTGGACACTCAGGAGGGTCAAAAGGAGACTTGGTGGCACC 1920
Db 1861 GGGAAAGAGAGACAATCGGCCCTGGACACTCAGGAGGGTCAAAAGGAGACTTGGTGGCACC 1920
QY 1921 ACTCATCTCTGCCACCCCGAGAATGCATCCTGCTCATCAGGTCCAGATTCTTTCCAAGG 1980
Db 1921 ACTCATCTCTGCCACCCCGAGAATGCATCCTGCTCATCAGGTCCAGATTCTTTCCAAGG 1980
QY 1981 CGGACGTTTTCTGTGGAATTTCTTAGTCTTGGCCCTCGGACACCTTCATTCTGTTAGCTGG 2040
Db 1981 CGGACGTTTTCTGTGGAATTTCTTAGTCTTGGCCCTCGGACACCTTCATTCTGTTAGCTGG 2040
QY 2041 GGAGTGGTGGTGAGGCAGTGAAGAAGAGCGGATGGTCACTCAGATCCACAGAGCCCCA 2100
Db 2041 GGAGTGGTGGTGAGGCAGTGAAGAAGAGCGGATGGTCACTCAGATCCACAGAGCCCCA 2100
QY 2101 GGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGGCCCCCACCACCCCTGCAC 2160

Db 2101 GGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCACCCCTGCAC 2160
QY 2161 AGCCCTCATCCCTCTTTGGCTTGAGCCGTGAGAGGCCCTGTGCTGAGTGTCTGACCGAGA 2220
Db 2161 AGCCCTCATCCCTCTTTGGCTTGAGCCGTGAGAGGCCCTGTGCTGAGTGTCTGACCGAGA 2220
QY 2221 CACTCACAGCTTTGTTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACG 2280
Db 2221 CACTCACAGCTTTGTTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACG 2280
QY 2281 CTTGCACTCGGGCCCATCTGGGCTCATGCTCTCTCTCCTGCTATTGAATTAGTACCTAG 2340
Db 2281 CTTGCACTCGGGCCCATCTGGGCTCATGCTCTCTCTCCTGCTATTGAATTAGTACCTAG 2340
QY 2341 CTGCACACAGTATGTAGTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA 2395
Db 2341 CTGCACACAGTATGTAGTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA 2395

RESULT 5
ABK33594

ID ABK33594 standard; cDNA; 2395 BP.

XX

AC ABK33594;

XX

DT 08-MAY-2002 (first entry)

XX

DE cDNA encoding human PRO protein, Seq ID No 117.

XX

KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200208288-A2.

XX

PD 31-JAN-2002.

XX

PF 29-JUN-2001; 2001WO-US021066.

XX

PR 20-JUL-2000; 2000US-0219556P.

PR

PR 25-JUL-2000; 2000US-0220585P.

PR

PR 25-JUL-2000; 2000US-0220605P.

PR

PR 25-JUL-2000; 2000US-0220607P.

PR

PR 25-JUL-2000; 2000US-0220624P.

PR

PR 25-JUL-2000; 2000US-0220638P.

PR

PR 25-JUL-2000; 2000US-0220664P.

PR

PR 25-JUL-2000; 2000US-0220666P.

PR

PR 26-JUL-2000; 2000US-0220893P.

PR

PR 28-JUL-2000; 2000WO-US020710.

PR

PR 01-AUG-2000; 2000US-0222425P.

PR

PR 22-AUG-2000; 2000US-0227133P.

PR

PR 23-AUG-2000; 2000WO-US023522.

PR

PR 24-AUG-2000; 2000WO-US023328.

PR

PR 10-NOV-2000; 2000WO-US030873.

PR

PR 28-NOV-2000; 2000US-0253646P.

PR

PR 01-DEC-2000; 2000WO-US032678.

PR

PR 20-DEC-2000; 2000US-00747259.

PR

PR 20-DEC-2000; 2000WO-US034956.

PR

PR 28-FEB-2001; 2001WO-US006520.

PR

PR 01-MAR-2001; 2001WO-US006666.

PR

PR 22-MAR-2001; 2001US-00816744.

PR

PR 10-MAY-2001; 2001US-00854208.

PR

PR 10-MAY-2001; 2001US-00854280.

PR

PR 25-MAY-2001; 2001WO-US017092.

XX

(GETH) GENENTECH INC.

PI

Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI

Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX

DR WPI; 2002-172001/22.
DR P-PSDB; AAU83650.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT or liver tumor.
XX
PS Claim 2; Fig 117; 359pp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human PRO
CC protein coding sequences of the invention
XX
SQ Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;
Query Match 100.0%; Score 2395; DB 6; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGAGCCGGAAGCGCGCTGCAGCAGGGCGAGGCTCCAGGTGGGTTCGGCATC 60
DB 1 CCTGGAGCCGGAAGCGCGCTGCAGCAGGGCGAGGCTCCAGGTGGGTTCGGCATC 60
QY 61 CAGCCTAGCGTGTCCACGATCGCGTCTCCCTCGGGGATTCCTCCGGCTCCCGTAGCG 120
DB 61 CAGCCTAGCGTGTCCACGATCGCGTCTCCCTCGGGGATTCCTCCGGCTCCCGTAGCG 120
QY 121 ATCGAGGTGCTAGGGATCGCGTCTCCCTCGGGGATTCCTCCGGCTCCCGTAGCGTCC 180
DB 121 ATCGAGGTGCTAGGGATCGCGTCTCCCTCGGGGATTCCTCCGGCTCCCGTAGCGTCC 180
QY 181 TCTGCCAGACGGGAACACGAGCGGAGCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
DB 181 TCTGCCAGACGGGAACACGAGCGGAGCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
QY 241 TCTAACTGGACCAACGCTGCCACCACTCTCTTCAGTAAAGTTGTTATTTCTGATAGAT 300
DB 241 TCTAACTGGACCAACGCTGCCACCACTCTCTTCAGTAAAGTTGTTATTTCTGATAGAT 300
QY 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGGTGTGAATTTATGCCCTACACAAC 360
DB 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGGTGTGAATTTATGCCCTACACAAC 360
QY 361 TACCTTGTAAGAAAGAGGATCTCACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT 420
DB 361 TACCTTGTAAGAAAGAGGATCTCACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT 420
QY 421 ACTATGCTCGAATCAAGGCATTTGATGACGGGAGCCCTTCCCTGGCTTGTGACGTCA 480
DB 421 ACTATGCTCGAATCAAGGCATTTGATGACGGGAGCCCTTCCCTGGCTTGTGACGTCA 480
QY 481 AGGAACCTCAATTCTCCTGCACCTGCTGGAAGACAGTGTGATAAGCAAGCAAGCAGCT 540
DB 481 AGGAACCTCAATTCTCCTGCACCTGCTGGAAGACAGTGTGATAAGCAAGCAAGCAGCT 540
QY 541 GGAAAAAGAAAGTAGTCTTTTATGGAGATGAACCTGGGTAAATTTATCCAAAGCATTTT 600
DB 541 GGAAAAAGAAAGTAGTCTTTTATGGAGATGAACCTGGGTAAATTTATCCAAAGCATTTT 600

QY 601 GTGGAATATGATGGAAACAACCTCATTTTTCGTGTGAGATTACACAGAGGTGGATAATAAT 660
DB 601 GTGGAATATGATGGAAACAACCTCATTTTTCGTGTGAGATTACACAGAGGTGGATAATAAT 660
QY 661 GTCACGAGGCATTTGGATAAAGTATTAAAAAGAGGAGATTGGACATATTAAATCCTCCAC 720
DB 661 GTCACGAGGCATTTGGATAAAGTATTAAAAAGAGGAGATTGGACATATTAAATCCTCCAC 720
QY 721 TACCTGGGCTGGACCACCATTTGGCCACATTTTTCAGGGCCCAACAGCCCTGATTGGGCAG 780
DB 721 TACCTGGGCTGGACCACCATTTGGCCACATTTTTCAGGGCCCAACAGCCCTGATTGGGCAG 780
QY 781 AAGCTGACGAGATGGACAGCGTCTGATGAAGATCCACACCTACTGCAGTCGAAGGAG 840
DB 781 AAGCTGACGAGATGGACAGCGTCTGATGAAGATCCACACCTACTGCAGTCGAAGGAG 840
QY 841 AGAGAGACGCTTTTACCAATTTTCTGCTGTTTCTTGTGGTGACCATGGCATGTCTGAAACA 900
DB 841 AGAGAGACGCTTTTACCAATTTTCTGCTGTTTCTTGTGGTGACCATGGCATGTCTGAAACA 900
QY 901 GGAAGTCAAGGGCTCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCT 960
DB 901 GGAAGTCAAGGGCTCTCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCT 960
QY 961 GCGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGCACGTCCTCAATAGACGGATGTG 1020
DB 961 GCGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGCACGTCCTCAATAGACGGATGTG 1020
QY 1021 GCTCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGAGCCTC 1080
DB 1021 GCTCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGAGCCTC 1080
QY 1081 CTATTCCCAGTTGTGGAAGGAAGACCAATAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
DB 1081 CTATTCCCAGTTGTGGAAGGAAGACCAATAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
QY 1141 ACAGTGCAGCTTAGTAAACTGTTGCAAGAGATGTCGCGTTCATATGAAAAAGATCCTGGG 1200
DB 1141 ACAGTGCAGCTTAGTAAACTGTTGCAAGAGATGTCGCGTTCATATGAAAAAGATCCTGGG 1200
QY 1201 TTTGAGCAGTTTAAATGTGCAAGAAAGATTGCAATGGGAATGGATCAGACTGTACTTGGAG 1260
DB 1201 TTTGAGCAGTTTAAATGTGCAAGAAAGATTGCAATGGGAATGGATCAGACTGTACTTGGAG 1260
QY 1261 GAAAGCATTTCAGAAAGTCTTATCAACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT 1320
DB 1261 GAAAGCATTTCAGAAAGTCTTATCAACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT 1320
QY 1321 GCTCTGAAGACGCTGAGTGTCTTCTGAGTGCAAGTGGCCCTGCTCACCCTGCTCC 1380
DB 1321 GCTCTGAAGACGCTGAGTGTCTTCTGAGTGCAAGTGGCCCTGCTCACCCTGCTCC 1380
QY 1381 TGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGTGGAAAGTCCCACCTGTCATCTC 1440
DB 1381 TGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGTGGAAAGTCCCACCTGTCATCTC 1440
QY 1441 CTGGGTTTCTCTGCTCTTTTATTTGGTGATCCTGGTCTTTCGGCCGTTTTCAGTCAATG 1500
DB 1441 CTGGGTTTCTCTGCTCTTTTATTTGGTGATCCTGGTCTTTCGGCCGTTTTCAGTCAATG 1500
QY 1501 TGTGCACTCAGCTGAAAGTTCGTCTACTTCTGTGGCCCTCTCGTGGCTGGCGGAGGCT 1560
DB 1501 TGTGCACTCAGCTGAAAGTTCGTCTACTTCTGTGGCCCTCTCGTGGCTGGCGGAGGCT 1560
QY 1561 GCCTTTCGTTTACCAGACTCTGGTTGAACACCTGTTGTCGAAGTCTGGCAGTGCCCC 1620
DB 1561 GCCTTTCGTTTACCAGACTCTGGTTGAACACCTGTTGTCGAAGTCTGGCAGTGCCCC 1620
QY 1621 TGGACAGGGGCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCTCTGGGTGTCCTC 1680
DB 1621 TGGACAGGGGCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCTCTGGGTGTCCTC 1680
QY 1681 GACACAGGTGTTCAATCTGTGTCTGTCAGGTGATGCCTCAGTTCTTGGAAAGCTAGGT 1740

PR 09-JUL-2001; 2001WO-US021735.
XX (GETH) GENENTECH INC.
PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
PI WPI; 2002-731348/79.
DR P-PSDB; ABG95920.
DR
XX
PT New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX
PS Claim 2; Fig 139; 399pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, C/G, D/H or E/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence encodes a novel secreted or transmembrane protein of the
CC invention
XX
SQ Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;
Query Match 100.0%; Score 2395; DB 6; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGAGCCGGAAGCGCGCTGCAGAGGGCGAGGCTCCAGGTGGGTCCGGTCCGCATC 60
Db |||||||
QY 61 CAGCCTAGCGTGTCCACGATCGGGCTCCGGGACTTTCGCTACCTGTTCCGTAGCG 120
Db |||||||
QY 61 CAGCCTAGCGTGTCCACGATCGGGCTCCGGGACTTTCGCTACCTGTTCCGTAGCG 120
QY 121 ATCAGGTCGTAGGATCGGGTCTTCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCC 180

Db 121 ATCAGGTCGTAGGATCGGGTCTTCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCC 180
QY 181 TCTGCCAGAGCGGAACACAGGAGCGGAGCCCCAGCGGCCGAAACCCCTCGGCTGGAGCCAGT 240
Db 181 TCTGCCAGAGCGGAACACAGGAGCGGAGCCCCAGCGGCCGAAACCCCTCGGCTGGAGCCAGT 240
QY 241 TCTAACTGGACCACGCTGCCACCACCTCTCTTTCAGTAAAGTTGTTATTGTTCTGATAGAT 300
Db 241 TCTAACTGGACCACGCTGCCACCACCTCTCTTTCAGTAAAGTTGTTATTGTTCTGATAGAT 300
QY 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAAC 360
Db 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAAC 360
QY 361 TACCTTGTGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAAGCCACCTACAGTT 420
Db 361 TACCTTGTGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAAGCCACCTACAGTT 420
QY 421 ACTATGCTCGAATCAAGGCAATGATGACGGGAGCCCTTCTCGCTTGTGACGTCATC 480
Db 421 ACTATGCTCGAATCAAGGCAATGATGACGGGAGCCCTTCTCGCTTGTGACGTCATC 480
QY 481 AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGACAAAGCAGCT 540
Db 481 AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGACAAAGCAGCT 540
QY 541 GGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTAAATTTATCCCAAGCATTTT 600
Db 541 GGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTAAATTTATCCCAAGCATTTT 600
QY 601 GTGGAATATGATGGAACCAACCTCATTTTCTGTGATTAACACAGAGTGGATAATAAT 660
Db 601 GTGGAATATGATGGAACCAACCTCATTTTCTGTGATTAACACAGAGTGGATAATAAT 660
QY 661 GTCACGAGGCAATTTGGATAAAGTATTAAGAGAGGAGATTGGGACATATTAATCTCCAC 720
Db 661 GTCACGAGGCAATTTGGATAAAGTATTAAGAGAGGAGATTGGGACATATTAATCTCCAC 720
QY 721 TACCTGGGCTGGACACATTTGGCCACATTTTTCAGGGCCCCAACAGCCCCCTGATGGG 780
Db 721 TACCTGGGCTGGACACATTTGGCCACATTTTTCAGGGCCCCAACAGCCCCCTGATGGG 780
QY 781 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAG 840
Db 781 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAG 840
QY 841 AGAGAGACGCTTTTACCCAATTTGCTGGTCTTCTTGTGGTACCATGGCATGTCTGAACA 900
Db 841 AGAGAGACGCTTTTACCCAATTTGCTGGTCTTCTTGTGGTACCATGGCATGTCTGAACA 900
QY 901 GGAAGTCACGGGGCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCT 960
Db 901 GGAAGTCACGGGGCTCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCT 960
QY 961 GCCTTTGAAAGGAAACCCCGTGATATCCGACATCCAAAGCAGTCCCAATAGACGGATGTG 1020
Db 961 GCCTTTGAAAGGAAACCCCGTGATATCCGACATCCAAAGCAGTCCCAATAGACGGATGTG 1020
QY 1021 GCTGCGACACTGGCGATAGCACTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC 1080
Db 1021 GCTGCGACACTGGCGATAGCACTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC 1080
QY 1081 CTATTCACAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
Db 1081 CTATTCACAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
QY 1141 ACAGTGACAGCTTAGTAAACTGTTGCAAGAGAATGTGCCGTATATGAAAAAGATCCTGGG 1200
Db 1141 ACAGTGACAGCTTAGTAAACTGTTGCAAGAGAATGTGCCGTATATGAAAAAGATCCTGGG 1200
QY 1201 TTTGAGCAGTTTAAATGTGAGAAAGATTCATGGGAACGTGGATCAGACTGTACTTGGAG 1260
Db 1201 TTTGAGCAGTTTAAATGTGAGAAAGATTCATGGGAACGTGGATCAGACTGTACTTGGAG 1260

Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
WPI; 2002-090516/12.
P-PSDB; ABB84962.
One hundred and eighty seven nucleic acids encoding PRO polypeptides,
useful in diagnosis and treatment of cardiovascular (e.g. myocardial
infarction), endothelial or angiogenic disorders in a mammal.
Claim 2; Fig 291; 565pp; English.
ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
activities, and can be used in gene therapy. The PRO polynucleotides,
proteins, agonists and antagonists are useful for treating or diagnosing
a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
angiogenesis (such as breast carcinoma and liver carcinoma) and wound
healing. The PRO polynucleotides have applications in molecular biology,
including use as hybridisation probes, and in chromosome and gene
mapping. ABL88259 to ABL88267 represent primers and probes used in the
exemplification of the present invention
Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;
Query Match 100.0%; Score 2395; DB 6; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CCTGGAGCCGGAAGCGCGCTGCAGCAGCGGAGGCTCCAGGTGGGTCCGTTCCGCATC 60
1 CCTGGAGCCGGAAGCGCGCTGCAGCAGCGGAGGCTCCAGGTGGGTCCGTTCCGCATC 60
61 CAGCCTAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTCGCTACCTGTTGGTAGCG 120
61 CAGCCTAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTCGCTACCTGTTGGTAGCG 120
121 ATCGAGGTGCTAGGGATCGCGGTCTTCCCTCGGGGATTTCTCCCGGCTCCCGTTCCGTTCC 180
121 ATCGAGGTGCTAGGGATCGCGGTCTTCCCTCGGGGATTTCTCCCGGCTCCCGTTCCGTTCC 180
181 TCTGCCAGAGCGGAACACGAGCGGAGCCCGGAGCCCGGAGCCCGGAGCCCGGAGT 240
181 TCTGCCAGAGCGGAACACGAGCGGAGCCCGGAGCCCGGAGCCCGGAGCCCGGAGT 240
241 TCTAACTGGACACCGCTGCCACACCTCTCTTCAAGTAAAGTTGTTATTTCTGATAGAT 300
241 TCTAACTGGACACCGCTGCCACACCTCTCTTCAAGTAAAGTTGTTATTTCTGATAGAT 300
301 GCCTTGAGAGATGATTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAAT 360
301 GCCTTGAGAGATGATTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAAT 360
361 TACCTTGTGGAAGAGGAGCATCTCAGATTTTGTGGCTGAAGCAAGCCACCTACAGTT 420
361 TACCTTGTGGAAGAGGAGCATCTCAGATTTTGTGGCTGAAGCAAGCCACCTACAGTT 420
421 ACTATGCTCGAATCAAGGCATTGATGACGGGAGCCTTCCCTGGCTTGTGACGTCATC 480
421 ACTATGCTCGAATCAAGGCATTGATGACGGGAGCCTTCCCTGGCTTGTGACGTCATC 480
481 AGGAACCTCAATTTCTCCTGCACTGCTGGAAGACAGTGTGATAAGACAAAGCAAGCAGCT 540
481 AGGAACCTCAATTTCTCCTGCACTGCTGGAAGACAGTGTGATAAGACAAAGCAAGCAGCT 540
541 GGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTTAAATTTATCCAAAGCATTTT 600
541 GGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTTAAATTTATCCAAAGCATTTT 600
601 GTGGAATATGATGGAAACAACCTCATTTTTCGTGCAGATTACACAGAGGTGGATAATAAT 660

601 GTGGAATATGATGGAAACAACCTCATTTTTCGTGCAGATTACACAGAGGTGGATAATAAT 660
661 GTCACGAGGCATTTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAATCCTCCAC 720
661 GTCACGAGGCATTTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAATCCTCCAC 720
721 TACCTGGGGCTGGACCAATTTGGCCACATTTTTCAGGGCCCAACAGCCCCCTGATTGGGAG 780
721 TACCTGGGGCTGGACCAATTTGGCCACATTTTTCAGGGCCCAACAGCCCCCTGATTGGGAG 780
781 AAGCTGAGCGAGATGGACAGCGCTGCTGATGAAGATCCACACCTCAGTCGAGTGAAGGAG 840
781 AAGCTGAGCGAGATGGACAGCGCTGCTGATGAAGATCCACACCTCAGTCGAGTGAAGGAG 840
841 AGAGAGAGCGCTTTTACCCAATTTTGTGGTGTGACCATGGCATGTCTGAAACA 900
841 AGAGAGAGCGCTTTTACCCAATTTTGTGGTGTGACCATGGCATGTCTGAAACA 900
901 GGAAGTCAAGCGGCGCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT 960
901 GGAAGTCAAGCGGCGCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT 960
961 GCGTTTGAAGGAAACCCCGGTGATATCCGACATCCAAAGCACGTCCTCAATAGACGGATGTG 1020
961 GCGTTTGAAGGAAACCCCGGTGATATCCGACATCCAAAGCACGTCCTCAATAGACGGATGTG 1020
1021 GCTGCGACACTGCGGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC 1080
1021 GCTGCGACACTGCGGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC 1080
1081 CTATTTCCAGTTTGTGAAGGAAGACCAATAGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
1081 CTATTTCCAGTTTGTGAAGGAAGACCAATAGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
1141 ACAGTGCAGTTTGTGAAGGAAGACCAATAGAGAGAGTGTCCGTCATATGAAAAAGATCCTGGG 1200
1141 ACAGTGCAGTTTGTGAAGGAAGACCAATAGAGAGAGTGTCCGTCATATGAAAAAGATCCTGGG 1200
1201 TTTGAGCAGTTTAAAAATGTCAGAAAGATTGTCATGGGAATGGATCAGACTGTACTTTGGAG 1260
1201 TTTGAGCAGTTTAAAAATGTCAGAAAGATTGTCATGGGAATGGATCAGACTGTACTTTGGAG 1260
1261 GAAAAAGCATTCAGAAAGTCTTATCAACCTGGGCTCCAAAGTTCTCAGGAGTACCTGGAT 1320
1261 GAAAAAGCATTCAGAAAGTCTTATCAACCTGGGCTCCAAAGTTCTCAGGAGTACCTGGAT 1320
1321 GCTCTGAAGACGCTGAGCTTGTCTCCCTGAGTGCACAAAGTGGCCCGGCTTCTCACCTGCTCC 1380
1321 GCTCTGAAGACGCTGAGCTTGTCTCCCTGAGTGCACAAAGTGGCCCGGCTTCTCACCTGCTCC 1380
1381 TGCTCAGCGTCCCAACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACTGTATCTC 1440
1381 TGCTCAGCGTCCCAACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACTGTATCTC 1440
1441 CTGGGTTTCTCTGCTCTTTTATTTTGGTGATCCTGGTCTTTTCGGCCGTTTCACGTCATTG 1500
1441 CTGGGTTTCTCTGCTCTTTTATTTTGGTGATCCTGGTCTTTTCGGCCGTTTCACGTCATTG 1500
1501 TGTGCACTCAGCTGAAAGTTCGTTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGAGGCT 1560
1501 TGTGCACTCAGCTGAAAGTTCGTTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGAGGCT 1560
1561 GCCTTTCTGTTTACAGACTCTGGTTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCC 1620
1561 GCCTTTCTGTTTACAGACTCTGGTTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCC 1620
1621 TGGACAGGGGCGCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCTCTGGGTGTCCC 1680
1621 TGGACAGGGGCGCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCTCTGGGTGTCCC 1680
1681 GACACAGGTGTTACATCTGTGCTGTGTCAGGTGAGATGCCTCAGTTCTTGGAAAGCTAGGT 1740
1681 GACACAGGTGTTACATCTGTGCTGTGTCAGGTGAGATGCCTCAGTTCTTGGAAAGCTAGGT 1740

Db 1681 GACACAGGTGTTACATCTGTGTGTGCTCAGGTCAGATGCCTCAGTTCTTGGAAAGCTAGGT 1740
QY 1741 TCCTGCGACTGTTACCAAGGTGATTGTAAGAGCTGGCGGTACAGAGGAACAAGCCCCC 1800
Db 1741 TCCTGCGACTGTTACCAAGGTGATTGTAAGAGCTGGCGGTACAGAGGAACAAGCCCCC 1800
QY 1801 CAGCTGAGGGGTGTGTGAATCGGACAGCTCCAGCAGAGGTGTGGAGTGCAGCTGA 1860
Db 1801 CAGCTGAGGGGTGTGTGAATCGGACAGCTCCAGCAGAGGTGTGGAGTGCAGCTGA 1860
QY 1861 GGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAAGGAGACTTGTTCGAAG 1920
Db 1861 GGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAAGGAGACTTGTTCGAAG 1920
QY 1921 ACTCATCTGCCACCCCCAGAAATGTCATCTGCTCGGACACTCAGGTCAGATTTCTTCCAAG 1980
Db 1921 ACTCATCTGCCACCCCCAGAAATGTCATCTGCTCGGACACTCAGGTCAGATTTCTTCCAAG 1980
QY 1981 CGGACGTTTCTGTTGGAAATCTTAGTCTTGGCCTCGGACACCTTCATTCGTTAGCTGG 2040
Db 1981 CGGACGTTTCTGTTGGAAATCTTAGTCTTGGCCTCGGACACCTTCATTCGTTAGCTGG 2040
QY 2041 GGAGTGGTGGTGAGGCGAGTGAAGAAGAGCGGATGGTCACACTCAGATCCACAGAGCCCA 2100
Db 2041 GGAGTGGTGGTGAGGCGAGTGAAGAAGAGCGGATGGTCACACTCAGATCCACAGAGCCCA 2100
QY 2101 GGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCACCCCTGCAC 2160
Db 2101 GGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCACCCCTGCAC 2160
QY 2161 AGCCCTCATCCCCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGTCTGACCGAGA 2220
Db 2161 AGCCCTCATCCCCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGTCTGACCGAGA 2220
QY 2221 CACTCACAGCTTTGTCTATCAGGGCACAGGCTTCTCGAGCCAGGATGATCTGTGCCAG 2280
Db 2221 CACTCACAGCTTTGTCTATCAGGGCACAGGCTTCTCGAGCCAGGATGATCTGTGCCAG 2280
QY 2281 CTTGCACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG 2340
Db 2281 CTTGCACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG 2340
QY 2341 CTGCACACAGTATGTAGTTACAAAAGATAAAGCAATAATTGAGAAAAAAA 2395
Db 2341 CTGCACACAGTATGTAGTTACAAAAGATAAAGCAATAATTGAGAAAAAAA 2395

RESULT 8
ABL95706

ID ABL95706 standard; cDNA; 2395 BP.

AC ABL95706;

XX ABL95706;

DT 19-JUL-2002 (first entry)

XX Human angiogenesis related cDNA PRO4405 SEQ ID NO: 291.

DE Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; Gene therapy; endothelial disorder;
KW cardiant; cytosstatic; antiangiogenic; hypotensive; vulnery;
KW antiarteriosclerotic; gene; ss.

OS Homo sapiens.

XX WO200208284-A2.

PN 31-JAN-2002.

PD 09-JUL-2001; 2001WO-US021735.

XX 20-JUL-2000; 2000US-0219556P.

PF 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220664P.

PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.

XX (GETH) GENENTECH INC.

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PA (WOOD/) WOOD W I.

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-171999/22.

DR P-PSDB; ABB95568.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.

PS Claim 1; Fig 291; 567pp; English.

XX The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention

XX Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;

Query Match									
Best Local Similarity 100.0%; Score 2395; DB 6; Length 2395;									
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	CCTGGAGCCGGAAGCGCGGCTGCAGCAGGCGGAGGCTCCAGGTGGGTTCGGTCCGCATC	60						
Db	1	CCTGGAGCCGGAAGCGCGGCTGCAGCAGGCGGAGGCTCCAGGTGGGTTCGGTCCGCATC	60						
QY	61	CAGCCTAGCGTGTCCACGATCGGCTGGCTCCGGGACTTCCGTAACCTGTTGGGTAGCG	120						
Db	61	CAGCCTAGCGTGTCCACGATCGGCTGGCTCCGGGACTTCCGTAACCTGTTGCGTAGCG	120						
QY	121	ATCGAGGTGCTAGGGATCGCGTCTTCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCC	180						
Db	121	ATCGAGGTGCTAGGGATCGCGTCTTCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCC	180						
QY	181	TCTGCCAGAGCGGAACAACGAGCGGAGCCCCAGCGCCGAAACCTCGGCTGGAGCCAGT	240						
Db	181	TCTGCCAGAGCGGAACAACGAGCGGAGCCCCAGCGCCGAAACCTCGGCTGGAGCCAGT	240						
QY	241	TCTAACTGGACACAGCTGCCACCACTCTCTTCAGTAAAGTTGTTATGTTCTGATAGAT	300						
Db	241	TCTAACTGGACACAGCTGCCACCACTCTCTTCAGTAAAGTTGTTATGTTCTGATAGAT	300						
QY	301	GCCTTGAGAGATGATTTTGTGTTGGGTCAAGGGTGTGAAATTTATGSCCTACACAAC	360						
Db	301	GCCTTGAGAGATGATTTTGTGTTGGGTCAAGGGTGTGAAATTTATGSCCTACACAAC	360						
QY	361	TACCTTGTTGGAAGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT	420						
Db	361	TACCTTGTTGGAAGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT	420						
QY	421	ACTATGCCCTCGAATCAAGGCATTGATGACGGGAGGCTTCTGGCTTTGTGCAAGCTCATC	480						
Db	421	ACTATGCCCTCGAATCAAGGCATTGATGACGGGAGGCTTCTGGCTTTGTGCAAGCTCATC	480						
QY	481	AGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGATAAGCAAGCAAGCAGCT	540						
Db	481	AGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGATAAGCAAGCAAGCAGCT	540						
QY	541	GGAAAAGAAATAGTCTTTTATGGAGATGAAACCTGGGTAAATATTCCCAAAGCAATTTT	600						
Db	541	GGAAAAGAAATAGTCTTTTATGGAGATGAAACCTGGGTAAATATTCCCAAAGCAATTTT	600						
QY	601	GTGGAATATGATGGAACAACCTCAATTTTCGTGTCAGATTACACAGAGGTGGATAATAT	660						
Db	601	GTGGAATATGATGGAACAACCTCAATTTTCGTGTCAGATTACACAGAGGTGGATAATAT	660						
QY	661	GTACAGAGGCATTTGGATAAAGTATTAAAAGAGGAGATTGGGCATATTAATCCTCCAC	720						
Db	661	GTACAGAGGCATTTGGATAAAGTATTAAAAGAGGAGATTGGGCATATTAATCCTCCAC	720						
QY	721	TACCTGGGGCTGGACCAACATTTGGCCACATTTAGGGCCCAACAGCCCCCTGATTGGGCAG	780						
Db	721	TACCTGGGGCTGGACCAACATTTGGCCACATTTAGGGCCCAACAGCCCCCTGATTGGGCAG	780						
QY	781	AAGCTGAGCGGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCACTCGAAGGAG	840						
Db	781	AAGCTGAGCGGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCACTCGAAGGAG	840						
QY	841	AGAGAGACGCTTTACCCAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACA	900						
Db	841	AGAGAGACGCTTTTACCCAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACA	900						
QY	901	GGAAAGTACGGGGCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCT	960						
Db	901	GGAAAGTACGGGGCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCT	960						
QY	961	GCCTTTGAAAGGAAACCCGGTGATATCCGACATCCAAAGCAGCTCCAAATAGACGGATG	1020						
Db	961	GCCTTTGAAAGGAAACCCGGTGATATCCGACATCCAAAGCAGCTCCAAATAGACGGATG	1020						

QY	1021	GCTGCGACACTGGCGATAGCACCTTGGCTTACCGATTCCAAAAGACAGTGTAGGAGCCTC	1080
Db	1021	GCTGCGACACTGGCGATAGCACCTTGGCTTACCGATTCCAAAAGACAGTGTAGGAGCCTC	1080
QY	1081	CTATTTCCAGTTGTGGAAGAACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT	1140
Db	1081	CTATTTCCAGTTGTGGAAGAACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT	1140
QY	1141	ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAAATGTCCTCATATGAAAAGATCCTGGG	1200
Db	1141	ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAAATGTCCTCATATGAAAAGATCCTGGG	1200
QY	1201	TTTGAGCAGTTTAAATGTGAGAAAGATTGCAATGGGAACTGGATCAGACTGTACTTGGAG	1260
Db	1201	TTTGAGCAGTTTAAATGTGAGAAAGATTGCAATGGGAACTGGATCAGACTGTACTTGGAG	1260
QY	1261	GAAAAGCATTCAGAAAGTCTTATTTCAACCTGGGCTCCAAAGTTCTCAGGCAGTACCTGGAT	1320
Db	1261	GAAAAGCATTCAGAAAGTCTTATTTCAACCTGGGCTCCAAAGTTCTCAGGCAGTACCTGGAT	1320
QY	1321	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCCAAGTTCTCACCTGCTCC	1380
Db	1321	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCCAAGTTCTCACCTGCTCC	1380
QY	1381	TGCTCAGCGTCCCACAGGCACCTGCACAGAAAGGCTGAGCTGGAACTCCCACTGTCTATCTC	1440
Db	1381	TGCTCAGCGTCCCACAGGCACCTGCACAGAAAGGCTGAGCTGGAACTCCCACTGTCTATCTC	1440
QY	1441	CTGGGTTTTCTCTGCTCTTTTATTTTGGTGAATCTGCTTCTTTCGGCCGTTACGTCATTG	1500
Db	1441	CTGGGTTTTCTCTGCTCTTTTATTTTGGTGAATCTGCTTCTTTCGGCCGTTACGTCATTG	1500
QY	1501	TGTGCACCTCAGCTGAAAGTTCTGCTACTTTCTGTGGCCTCTCGTGGCTGGCGCAGGCT	1560
Db	1501	TGTGCACCTCAGCTGAAAGTTCTGCTACTTTCTGTGGCCTCTCGTGGCTGGCGCAGGCT	1560
QY	1561	GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGTGTGTCGCAAGTCTGCGCAGTGCCC	1620
Db	1561	GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGTGTGTCGCAAGTCTGCGCAGTGCCC	1620
QY	1621	TGGACAGGGGGCTCAGGGAAGGACGTTGAGCAGCCTTATCCAGGCTCTGGGTGTCCC	1680
Db	1621	TGGACAGGGGGCTCAGGGAAGGACGTTGAGCAGCCTTATCCAGGCTCTGGGTGTCCC	1680
QY	1681	GACACAGGTGTTTACATCTGTGCTGTGAGGAGCTGAGGAGCTTATCCAGGCTCTGGGTGTCCC	1740
Db	1681	GACACAGGTGTTTACATCTGTGCTGTGAGGAGCTGAGGAGCTTATCCAGGCTCTGGGTGTCCC	1740
QY	1741	TCCTGCGACTGTTTACAAAGGTGTTTAAAGAGCTGGCGGTACAGAGGAAACAAGCCCC	1800
Db	1741	TCCTGCGACTGTTTACAAAGGTGTTTAAAGAGCTGGCGGTACAGAGGAAACAAGCCCC	1800
QY	1801	CAGCTGAGGGGGTGTGTAATCCGACAGCTCCAGAGGCTGCGGAGCTGCGAGCTGA	1860
Db	1801	CAGCTGAGGGGGTGTGTAATCCGACAGCTCCAGAGGCTGCGGAGCTGCGAGCTGA	1860
QY	1861	GGGAAGAGAGACAATCGGCTGGACACTCAGGAGGGTCAAAAGGAGACTTGGTCCGACC	1920
Db	1861	GGGAAGAGAGACAATCGGCTGGACACTCAGGAGGGTCAAAAGGAGACTTGGTCCGACC	1920
QY	1921	ACTCATCTCTGCCACCCCAAGATGCAATCCTGCTCATCAGGTCCAGATTTCTTCCAAAGG	1980
Db	1921	ACTCATCTCTGCCACCCCAAGATGCAATCCTGCTCATCAGGTCCAGATTTCTTCCAAAGG	1980
QY	1981	CGGACGTTTTCTGTGGAATTTCTTAGTCTTGGCTCGGACACCTTCATTCGTTAGCTGG	2040
Db	1981	CGGACGTTTTCTGTGGAATTTCTTAGTCTTGGCTCGGACACCTTCATTCGTTAGCTGG	2040
QY	2041	GGAGTGGTGGTGAGGAGGAGGAGGCGGATGTCACACTCAGATCCACAGAGCCCCA	2100
Db	2041	GGAGTGGTGGTGAGGAGGAGGAGGCGGATGTCACACTCAGATCCACAGAGCCCCA	2100
QY	2101	GGATCAAGGGAACCCACTGTCAGTGGCAGCAGGACTGTTGGGCCCCCAACCCCTGCAC	2160

Db 121 ATCGAGGTGCTAGGATCGCGTCTTCCCTCGGGATTCTTCCCGGCTCCCGTTCGTTCC 180
QY 181 TCTGCCAGAGCGGAACACAGGAGCGGAGCCGCCAGGCCCGAAACCTCGGCTCGAGCCAGT 240
Db 181 TCTGCCAGAGCGGAACACAGGAGCGGAGCCGCCAGGCCCGAAACCTCGGCTCGAGCCAGT 240
QY 241 TCTAACTGGACCAACCGCTGCCACCACTCTCTTCACTAAGATTGTTATTGTTCTGATAGAT 300
Db 241 TCTAACTGGACCAACCGCTGCCACCACTCTCTTCACTAAGATTGTTATTGTTCTGATAGAT 300
QY 301 GCTTGTGAGAGATGATTTTGTGTTGGGTCAAAGGGTGAAGATTATGCTTACCAACT 360
Db 301 GCTTGTGAGAGATGATTTTGTGTTGGGTCAAAGGGTGAAGATTATGCTTACCAACT 360
QY 361 TACCTTTGGAAGAGGAGCATCTACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT 420
Db 361 TACCTTTGGAAGAGGAGCATCTACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT 420
QY 421 ACTATGCTCGAATCAAGGCATTGATGACGGGAGCCTTCCCTGGCTTGTGACGTATC 480
Db 421 ACTATGCTCGAATCAAGGCATTGATGACGGGAGCCTTCCCTGGCTTGTGACGTATC 480
QY 481 AGAAACCTCAATTTCTCTGCACTGCTGGAACAGTGTGATAAGACAAAGCAAGCAGCT 540
Db 481 AGAAACCTCAATTTCTCTGCACTGCTGGAACAGTGTGATAAGACAAAGCAAGCAGCT 540
QY 541 GGAAGAAAGATAGTCTTTTATGGAGATGAACCTGGGTAAATTTATTTCCCAAGCATTTT 600
Db 541 GGAAGAAAGATAGTCTTTTATGGAGATGAACCTGGGTAAATTTATTTCCCAAGCATTTT 600
QY 601 GTGGAATATGATGGAACCAACCTCATTTTTCGTGTCAGATTACACAGAGGTGGATAAAT 660
Db 601 GTGGAATATGATGGAACCAACCTCATTTTTCGTGTCAGATTACACAGAGGTGGATAAAT 660
QY 661 GTCAAGAGGCAATTTGGATAAAGTATTAAGAGAGGAGATTGGGACATATTATCTCCAC 720
Db 661 GTCAAGAGGCAATTTGGATAAAGTATTAAGAGAGGAGATTGGGACATATTATCTCCAC 720
QY 721 TACCTGGGGCTGGACCAATTTGGCCCATTTTTCAGGGCCCAACAGCCCTGATTGGGAG 780
Db 721 TACCTGGGGCTGGACCAATTTGGCCCATTTTTCAGGGCCCAACAGCCCTGATTGGGAG 780
QY 781 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGAGTGAAGGAG 840
Db 781 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGAGTGAAGGAG 840
QY 841 AGAGAGACGCTTTTACCCAAATTTGCTGGTCTTGTGGTGACCATGCGATGCTGAACA 900
Db 841 AGAGAGACGCTTTTACCCAAATTTGCTGGTCTTGTGGTGACCATGCGATGCTGAACA 900
QY 901 GGAAGTCAACGGGGCTTCTCCACCGAGGAGGTGAATACACCTCTGATTTTATCAGTTCT 960
Db 901 GGAAGTCAACGGGGCTTCTCCACCGAGGAGGTGAATACACCTCTGATTTTATCAGTTCT 960
QY 961 GCGTTTGAAGAAACCCCGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTG 1020
Db 961 GCGTTTGAAGAAACCCCGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTG 1020
QY 1021 GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC 1080
Db 1021 GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC 1080
QY 1081 CTATTTCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
Db 1081 CTATTTCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
QY 1141 ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAAATGTGCCGTCAATGAAAAAGATCTCTGG 1200
Db 1141 ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAAATGTGCCGTCAATGAAAAAGATCTCTGG 1200
QY 1201 TTTGAGCAGTTTAAAAATGTGAGAAAGATTGATGGAACTGGATCAGACTGTACTTGGAG 1260

Db 1201 TTTGAGCAGTTTAAAAATGTGAGAAAGATTGATGGAACTGGATCAGACTGTACTTGGAG 1260
QY 1261 GAAAAGCATTCAGAAAGTCTATTCAACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT 1320
Db 1261 GAAAAGCATTCAGAAAGTCTATTCAACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT 1320
QY 1321 GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCAGTTCTCACCTGCTCC 1380
Db 1321 GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCAGTTCTCACCTGCTCC 1380
QY 1381 TGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACCTGCTATC 1440
Db 1381 TGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACCTGCTATC 1440
QY 1441 CTGGCTTTTCTCTGCTCTCTTTTATTTGTTGATCCTGGTTCTTTCGCGCTTACGTCATTG 1500
Db 1441 CTGGCTTTTCTCTGCTCTCTTTTATTTGTTGATCCTGGTTCTTTCGCGCTTACGTCATTG 1500
QY 1501 TGTGACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCTGCGCTGGCGGAGGCT 1560
Db 1501 TGTGACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCTGCGCTGGCGGAGGCT 1560
QY 1561 GCCTTTTCTGCTCTCTTTTATTTGTTGATCCTGGTTCTTTCGCGCTTACGTCATTG 1620
Db 1561 GCCTTTTCTGCTCTCTTTTATTTGTTGATCCTGGTTCTTTCGCGCTGGCGGAGGCT 1620
QY 1621 TGGACAGGGGCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCTCTGGGTGCTCC 1680
Db 1621 TGGACAGGGGCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCTCTGGGTGCTCC 1680
QY 1681 GACACAGGTGTTTACATCTGTGCTGTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1740
Db 1681 GACACAGGTGTTTACATCTGTGCTGTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1740
QY 1741 TCCTGCGACTGTTACCAAGTGAATTTAAAGAGCTGGCGGTCAAGAGGAAAGCAAGCC 1800
Db 1741 TCCTGCGACTGTTACCAAGTGAATTTAAAGAGCTGGCGGTCAAGAGGAAAGCAAGCC 1800
QY 1801 CAGCTGAGGGGTGTGTAATCGGACAGCTCCAGAGGCTGGAGCTGGAGCTGGAGCTGA 1860
Db 1801 CAGCTGAGGGGTGTGTAATCGGACAGCTCCAGAGGCTGGAGCTGGAGCTGGAGCTGA 1860
QY 1861 GGAAGAAAGACAAATCGGCTTGACACTCAGGAGGCTCAAAGGAGACTTGGTCGCACC 1920
Db 1861 GGAAGAAAGACAAATCGGCTTGACACTCAGGAGGCTCAAAGGAGACTTGGTCGCACC 1920
QY 1921 ACTATCTGCCACCCCAAGATGCTGCTGCTCATCAGGTCAGATTTCTTTCCAGG 1980
Db 1921 ACTATCTGCCACCCCAAGATGCTGCTGCTCATCAGGTCAGATTTCTTTCCAGG 1980
QY 1981 CGGACGTTTCTGTTGGAATTTCTTAGTCTTGGCTTGGCTCGGACACCTTCACTGCTGG 2040
Db 1981 CGGACGTTTCTGTTGGAATTTCTTAGTCTTGGCTTGGCTCGGACACCTTCACTGCTGG 2040
QY 2041 GGAGTGGTGGTGAAGAGAGGCGGATGGTCACTCAGATCCACAGAGCCCA 2100
Db 2041 GGAGTGGTGGTGAAGAGAGGCGGATGGTCACTCAGATCCACAGAGCCCA 2100
QY 2101 GGATCAAGGGACCCACTGAGTGGCAGGAGCTGTTGGGCCCCCAACCCCTGCAC 2160
Db 2101 GGATCAAGGGACCCACTGAGTGGCAGGAGCTGTTGGGCCCCCAACCCCTGCAC 2160
QY 2161 AGCCCTCATCCCTCTTGGCTTGGCTGAGCCGTGAGGCTGCTGAGTGTGACCGAGA 2220
Db 2161 AGCCCTCATCCCTCTTGGCTTGGCTGAGCCGTGAGGCTGCTGAGTGTGACCGAGA 2220
QY 2221 CACTCAGCTTTTGTATCAGGCAAGGCTTCTCGAGCCAGGATGATCTGTGCCACG 2280
Db 2221 CACTCAGCTTTTGTATCAGGCAAGGCTTCTCGAGCCAGGATGATCTGTGCCACG 2280
QY 2281 CTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
Db 2281 CTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340

QY 2341 CTGCACACAGTATGTAGTTACCAAAAGAAATAAACGGCAATAATTGAGAAAAAAA 2395
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2341 CTGCACACAGTATGTAGTTACCAAAAGAAATAAACGGCAATAATTGAGAAAAAAA 2395
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 10
ACA66899
ID ACA66899 standard; cDNA; 2395 BP.
XX
AC ACA66899;
XX
DT 23-JUN-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #59.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN US2003036635-A1.
XX
PD 20-FEB-2003.
XX
PF 28-AUG-2002; 2002US-00230163.
XX
PR 25-JUL-2000; 2000US-0220638P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-342045/32.
DR P-PSDB; ABU80797.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for the manufacture of a medicament for diagnosing or treating
PT tumor.
XX
PS Claim 2; Fig 117; 314pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
CC useful in diagnostic assays for PRO, by detecting its expression in
CC specific cells, tissues or serum, and for affinity purification of PRO
CC from recombinant cell culture or natural sources. ACA66841-ACA66962
CC represent cDNA sequences encoding the human PRO polypeptides of the
CC invention. Note: The sequence data for this patent was obtained in
CC electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDentry.html
XX
SQ Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;

Query Match
Best Local Similarity 100.0%; Score 2395; DB 7; Length 2395;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGAGCGGAAGCGGGCTGCAGCAGGCGGAGGCTCCAGGTGGGTTCGGTCGCATC 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 CCTGGAGCGGAAGCGGGCTGCAGCAGGCGGAGGCTCCAGGTGGGTTCGGTCGCATC 60
QY 61 CAGCCTAGCGTGTCCACGATCGGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCG 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 CAGCCTAGCGTGTCCACGATCGGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCG 120

QY 121 ATCAGAGTGTAGGGATCGCGTCTTCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCC 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 ATCAGAGTGTAGGGATCGCGTCTTCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCC 180
QY 181 TCTGCCAGAGCGGAACACGAGCGGAGCCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 TCTGCCAGAGCGGAACACGAGCGGAGCCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
QY 241 TCTAACTGGACCGCTGCCACCCCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGAT 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 TCTAACTGGACCGCTGCCACCCCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGAT 300
QY 301 GCCTTGAGAGATGATTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACT 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 GCCTTGAGAGATGATTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACT 360
QY 361 TACCTTGTGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAAGCCACCTACAGTT 420
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TACCTTGTGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAAGCCACCTACAGTT 420
QY 421 ACTATGCCTCGAATCAAGGCATTGATGACGGGAGCCTTCTCGGCTTGTGACGTCATC 480
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 ACTATGCCTCGAATCAAGGCATTGATGACGGGAGCCTTCTCGGCTTGTGACGTCATC 480
QY 481 AGGAACCTCAATTCTCTGCACTGCTGGAAGACAGTGTGATAAGCAAAAGCAGCT 540
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 AGGAACCTCAATTCTCTGCACTGCTGGAAGACAGTGTGATAAGCAAAAGCAGCT 540
QY 541 GGAATAAGAAATAGTCTTTTATGGAGATGAACCTGGTTAAATTTATCCAAAGCATTTT 600
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 GGAATAAGAAATAGTCTTTTATGGAGATGAACCTGGTTAAATTTATCCAAAGCATTTT 600
QY 601 GTGGAATATGATGGAACAACCTCATTTTTCGTGTGATGATGATGATGATGATGATGAT 660
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 GTGGAATATGATGGAACAACCTCATTTTTCGTGTGATGATGATGATGATGATGATGAT 660
QY 661 GTACGAGGCTGGAACCAATTTTAAAGAGGAGATTGGGACATATTATCTCTCCAC 720
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 GTACGAGGCTGGAACCAATTTTAAAGAGGAGATTGGGACATATTATCTCTCCAC 720
QY 721 TACCTGGGCTGGACCAATTTGCGGCTGATGATGATGATGATGATGATGATGATGATG 780
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 TACCTGGGCTGGACCAATTTGCGGCTGATGATGATGATGATGATGATGATGATGATG 780
QY 781 AAGCTGAGCGAGATGGACAGCGTGTGATGATGATGATGATGATGATGATGATGATGATG 840
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 AAGCTGAGCGAGATGGACAGCGTGTGATGATGATGATGATGATGATGATGATGATGATG 840
QY 841 AGAGAGACGCTTTTACCAATTTTGTGCTGTTCTTGTGGTGACCATGGCATGTCTGAAACA 900
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 AGAGAGACGCTTTTACCAATTTTGTGCTGTTCTTGTGGTGACCATGGCATGTCTGAAACA 900
QY 901 GGAAGTCACGGGGCTCTCCACCGGAGGAGTGAATACACCTCTGATTTTAATCAGTTCT 960
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
901 GGAAGTCACGGGGCTCTCTCCACCGGAGGAGTGAATACACCTCTGATTTTAATCAGTTCT 960
QY 961 GCGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGCACGTCCTCAATAGACGGATGTG 1020
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
961 GCGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGCACGTCCTCAATAGACGGATGTG 1020
QY 1021 GCTGCGACACTGGCGATAGCATTGGCTTACCGATTCCAAAGACAGTGTAGGAGCCTC 1080
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1021 GCTGCGACACTGGCGATAGCATTGGCTTACCGATTCCAAAGACAGTGTAGGAGCCTC 1080
QY 1081 CTATTCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTGAT 1140
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1081 CTATTCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTGAT 1140
QY 1141 ACAGTGCAGCTTAGTAACTGTTGCAAGAGAAATGTGCCGTATATGAAAAAGATCCTGGG 1200
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1141 ACAGTGCAGCTTAGTAACTGTTGCAAGAGAAATGTGCCGTATATGAAAAAGATCCTGGG 1200

CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. This sequence encodes a novel human secreted and transmembrane PRO
CC polypeptide
XX

SQ Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;

Query Match 100.0%; Score 2395; DB 7; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CCTGGAGCCGGAAGCGGCTGCAGCAGGCGCAGGCTCCAGGTGGGTCCGATC	60
Db	1	CCTGGAGCCGGAAGCGGCTGCAGCAGGCGCAGGCTCCAGGTGGGTCCGATC	60
QY	61	CAGCCTAGCGTGTCCACGATCGCGTGGCTCCGGGACTTTCGCTACCTGTTCCGTAGCG	120
Db	61	CAGCCTAGCGTGTCCACGATCGCGTGGCTCCGGGACTTTCGCTACCTGTTCCGTAGCG	120
QY	121	ATCGAGGTGCTAGGGATCGCGTCTTCTTCGGGGATTTCTCCCGGTCCCGTTCGTTCC	180
Db	121	ATCGAGGTGCTAGGGATCGCGTCTTCTTCGGGGATTTCTCCCGGTCCCGTTCGTTCC	180
QY	181	TCTGCCAGAGCGGAACACGGAGCGGAGCCCCCAGCGCCCGAACCTCGGCTGGAGCCAGT	240
Db	181	TCTGCCAGAGCGGAACACGGAGCGGAGCCCCCAGCGCCCGAACCTCGGCTGGAGCCAGT	240
QY	241	TCTAACTGGACCACCGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTTCTGATAGAT	300
Db	241	TCTAACTGGACCACCGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTTCTGATAGAT	300
QY	301	GCCTTGAGAGATGATTTTGTGTGTGGGTCAAAGGTTGTGAATTTATGCCCTACACAAC	360
Db	301	GCCTTGAGAGATGATTTTGTGTGTGGGTCAAAGGTTGTGAATTTATGCCCTACACAAC	360
QY	361	TACCTTGTGGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT	420
Db	361	TACCTTGTGGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT	420
QY	421	ACTATGCCCTCGAATCAAGGCATGATGACGGGAGCCCTTCTGGCTTGTGCGAGTCATC	480
Db	421	ACTATGCCCTCGAATCAAGGCATGATGACGGGAGCCCTTCTGGCTTGTGCGAGTCATC	480
QY	481	AGGAACCTCAATTCTCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCT	540
Db	481	AGGAACCTCAATTCTCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCT	540
QY	541	GGAAAAAGAATAGTCTTTTATGGAGATGAACCTGGGTAAATTTATCCAAAGCATTTT	600
Db	541	GGAAAAAGAATAGTCTTTTATGGAGATGAACCTGGGTAAATTTATCCAAAGCATTTT	600
QY	601	GTGGAATATGATGGAAACAACCTCATTTTTCGTGCAGATTACACAGAGGTGGATAATA	660
Db	601	GTGGAATATGATGGAAACAACCTCATTTTTCGTGCAGATTACACAGAGGTGGATAATA	660
QY	661	GTCACGAGGCAATTTGGATAAAGTATTAATAAGAGGAGATTGGGACATATTAATCCTCCAC	720
Db	661	GTCACGAGGCAATTTGGATAAAGTATTAATAAGAGGAGATTGGGACATATTAATCCTCCAC	720
QY	721	TACCTGGGCTGGACACATTTGGCCACATTTTCAGGGCCCCAACAGCCCCCTGATTGGGCG	780
Db	721	TACCTGGGCTGGACACATTTGGCCACATTTTCAGGGCCCCAACAGCCCCCTGATTGGGCG	780
QY	781	AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAGGAG	840
Db	781	AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAGGAG	840
QY	841	AGAGAGACGCTTTTACCCCAATTTGCTGGTCTTTTGTGGTGACCATGGCATGTCTGAAACA	900
Db	841	AGAGAGACGCTTTTACCCCAATTTGCTGGTCTTTTGTGGTGACCATGGCATGTCTGAAACA	900
QY	901	GGAGTCACGGGGCCTCCTCCACCGAGGAGTGAATACACCTCTGATTTTAATCAGTTCT	960

Db	901	GGAAGTCACGGGGCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTAATCAGTTCT	960
QY	961	GCGTTTGAAGGAACCCCGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTG	1020
Db	961	GCGTTTGAAGGAACCCCGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTG	1020
QY	1021	GCTGCGACACTGCGGATAGCACTTGGCTTACCGATTCGCTCATATGAAAAAGATCCTGGG	1080
Db	1021	GCTGCGACACTGCGGATAGCACTTGGCTTACCGATTCGCTCATATGAAAAAGATCCTGGG	1080
QY	1081	CTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT	1140
Db	1081	CTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT	1140
QY	1141	ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCCGTATATGAAAAAGATCCTGGG	1200
Db	1141	ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCCGTATATGAAAAAGATCCTGGG	1200
QY	1201	TTTGAGCAGTTTAAAAATGTCAGAAAGATTGTCATGGGAACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT	1260
Db	1201	TTTGAGCAGTTTAAAAATGTCAGAAAGATTGTCATGGGAACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT	1260
QY	1261	GAAAAGCAATTGAGAGTCCATTATTCACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT	1320
Db	1261	GAAAAGCAATTGAGAGTCCATTATTCACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT	1320
QY	1321	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCAACAAGTGGCCAGTTCTCACCCCTGCTCC	1380
Db	1321	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCAACAAGTGGCCAGTTCTCACCCCTGCTCC	1380
QY	1381	TGCTCAGCGTCCCAACAGGCACTGCACAGAAAGGTGAGTGGAAAGTCCCACTGTCTATCTC	1440
Db	1381	TGCTCAGCGTCCCAACAGGCACTGCACAGAAAGGTGAGTGGAAAGTCCCACTGTCTATCTC	1440
QY	1441	CTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCCTTCGGCCGTTTCAAGTATG	1500
Db	1441	CTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCCTTCGGCCGTTTCAAGTATG	1500
QY	1501	TGTGCACCTCAGCTGAAAGTTCGTCTACTTCTGTGSCCTCTCTGCTGGCTGGCGGAGGCT	1560
Db	1501	TGTGCACCTCAGCTGAAAGTTCGTCTACTTCTGTGSCCTCTCTGCTGGCTGGCGGAGGCT	1560
QY	1561	GCCTTTCGTTTACCAGACTCTGGTTGAACACCTGTGTGTGCCAAGTCTGGGAGTGCCCC	1620
Db	1561	GCCTTTCGTTTACCAGACTCTGGTTGAACACCTGTGTGTGCCAAGTCTGGGAGTGCCCC	1620
QY	1621	TGGACAGGGGCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCTCTGGGTGTCCC	1680
Db	1621	TGGACAGGGGCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCTCTGGGTGTCCC	1680
QY	1681	GACACAGGTGTTACATCTGTGCTGTCAGTGCAGATGCCTCAGTTCTTGAAAAGCTAGGT	1740
Db	1681	GACACAGGTGTTACATCTGTGCTGTCAGTGCAGATGCCTCAGTTCTTGAAAAGCTAGGT	1740
QY	1741	TCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCC	1800
Db	1741	TCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCC	1800
QY	1801	CAGCTGAGGGGTGTGTGAATCGGACAGCCTCCAGCAGAGGTGTGGAGCTGCAGCTGA	1860
Db	1801	CAGCTGAGGGGTGTGTGAATCGGACAGCCTCCAGCAGAGGTGTGGAGCTGCAGCTGA	1860
QY	1861	GGGAAGAAGAGACAATCGGCTGGACACTCAGGAGGTCAAAAGGAGACTTGGTCGCACC	1920
Db	1861	GGGAAGAAGAGACAATCGGCTGGACACTCAGGAGGTCAAAAGGAGACTTGGTCGCACC	1920
QY	1921	ACTCATCCTGCCACCCCCCAGAAATGCATCCTGCCTCATCAGTCCAGATTTCTTCCAAG	1980
Db	1921	ACTCATCCTGCCACCCCCCAGAAATGCATCCTGCCTCATCAGTCCAGATTTCTTCCAAG	1980
QY	1981	CGGACGTTTTCTGTGGAAATCTTAGTCTTGGCTCGGACACCTTCATTCGTTAGCTGG	2040

PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-447384/42.
DR P-PSDB; ABO34004.
XX
PT New isolated antibody specifically binding a PRO polypeptide, useful for
PT the preparation of a medicament for treating disorders with the aberrant
PT expression or activity of the PRO polypeptide, such as tumor conditions
PT and cancer.
XX
PS Disclosure; Fig 139; 223pp; English.
XX
XX The invention relates to an antibody that binds to a secreted or
CC transmembrane protein designated PRO1446 appearing as ABO33941. The
CC protein is one of 84 PRO polypeptides which (along with their encoding
CC nucleic acids) are disclosed in the specification. The methods and
CC compositions of the present invention are useful for the preparation of a
CC medicament for the treatment of disorders associated with the aberrant
CC expression or activity of the PRO polypeptide, such as tumour conditions
CC and cancer. They can also be used to generate transgenic or knockout
CC animals useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC molecular weight markers for protein electrophoresis, chromosome
CC identification and tissue typing. The antibodies may be used in various
CC diagnostic, competitive binding and/or immunoprecipitation assays. The
CC present sequence encodes a PRO polypeptide
XX
SQ Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;
Query Match 100.0%; Score 2395; DB 7; Length 2395;
Best local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGTCCGTTCCGCATC 60
Db 1 CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGTCCGTTCCGCATC 60
QY 61 CAGCCTAGCGTGTCACGATCGCGGTCTCCGGGACTTTCGTAACCTGTTGGGTAGCG 120
Db 61 CAGCCTAGCGTGTCACGATCGCGGTCTCCGGGACTTTCGTAACCTGTTGGGTAGCG 120
QY 121 ATCGAGGTGCTAGGGATCGCGGTCTTCTTCGGGGATTCCTCCGGCTCCCGTTCTTCC 180
Db 121 ATCGAGGTGCTAGGGATCGCGGTCTTCTTCGGGGATTCCTCCGGCTCCCGTTCTTCC 180
QY 181 TCTGCCAGAGCGGAACACGAGCGGAGCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
Db 181 TCTGCCAGAGCGGAACACGAGCGGAGCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
QY 241 TCTAACTGGACCAACGCTGCCACCACTCTCTTTCAGTAAAGTTGTTATTTCTGTATAGAT 300
Db 241 TCTAACTGGACCAACGCTGCCACCACTCTCTTTCAGTAAAGTTGTTATTTCTGTATAGAT 300
QY 301 GCCTTTGAGAGATGATTTTGTGTTGGGTCAAAGGGGTGTAATTTATGCCCTACACAACT 360
Db 301 GCCTTTGAGAGATGATTTTGTGTTGGGTCAAAGGGGTGTAATTTATGCCCTACACAACT 360
QY 361 TACCTTGTGAAAAAGGAGCATCTCAGTTTGTGGTGAAGCAAAAGCCACCTACAGTT 420
Db 361 TACCTTGTGAAAAAGGAGCATCTCAGTTTGTGGTGAAGCAAAAGCCACCTACAGTT 420

Db 361 TACCTTGTGAAAAAGGAGCATCTCAGTTTGTGGTGAAGCAAAAGCCACCTACAGTT 420
QY 421 ACTATGCCTCGAATCAAGGCATTGATGACGGGGAGCCTTCTGGCTTTGTGACGTCATC 480
Db 421 ACTATGCCTCGAATCAAGGCATTGATGACGGGGAGCCTTCTGGCTTTGTGACGTCATC 480
QY 481 AGGAACCTCAATTCTCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCT 540
Db 481 AGGAACCTCAATTCTCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCT 540
QY 541 GGAAAAAAGAATAGTCTTTTATGGAGATGAACCTGGGTTAAATATTATCCCAAAGCATTTT 600
Db 541 GGAAAAAAGAATAGTCTTTTATGGAGATGAACCTGGGTTAAATATTATCCCAAAGCATTTT 600
QY 601 GTGGAATATGATGGAACAACCTCATTTTTCGTGTCAGATTACACAGAGGTGGATAATAAT 660
Db 601 GTGGAATATGATGGAACAACCTCATTTTTCGTGTCAGATTACACAGAGGTGGATAATAAT 660
QY 661 GTCACGAGGCATTTGGATAAAAGTATTAAGAGAGGAGATTGGGACATATTAATCCTCCAC 720
Db 661 GTCACGAGGCATTTGGATAAAAGTATTAAGAGAGGAGATTGGGACATATTAATCCTCCAC 720
QY 721 TACCTGGGCTGGACCAATTTGGCCACATTTTTCAGGGCCCAACAGCCCTGATTGGGCG 780
Db 721 TACCTGGGCTGGACCAATTTGGCCACATTTTTCAGGGCCCAACAGCCCTGATTGGGCG 780
QY 781 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAG 840
Db 781 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAG 840
QY 841 AGAGAGACGCTTTACCCAAATTTGCTGGTCTTTTGTGGTACCAATGGCATGTCTGAAACA 900
Db 841 AGAGAGACGCTTTACCCAAATTTGCTGGTCTTTTGTGGTACCAATGGCATGTCTGAAACA 900
QY 901 GGAAGTCACGGGCTTCCACCGAGGAGGTGAATACACCTCTGATTTAATCAGTTCT 960
Db 901 GGAAGTCACGGGCTTCCACCGAGGAGGTGAATACACCTCTGATTTAATCAGTTCT 960
QY 961 GCGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGCACGTCCCAATAGACGGATGTG 1020
Db 961 GCGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGCACGTCCCAATAGACGGATGTG 1020
QY 1021 GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGAGCCTC 1080
Db 1021 GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGAGCCTC 1080
QY 1081 CTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGACAGTGTGAGATTTTACATTTGAAT 1140
Db 1081 CTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGACAGTGTGAGATTTTACATTTGAAT 1140
QY 1141 ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAAATGTCCCGTCATATGAAAAAGATCCTGGG 1200
Db 1141 ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAAATGTCCCGTCATATGAAAAAGATCCTGGG 1200
QY 1201 TTTGAGCAGTTTAAATGTGAGAAAGATTGCAATGGGAACTGGATCAGACTGTACTGGAG 1260
Db 1201 TTTGAGCAGTTTAAATGTGAGAAAGATTGCAATGGGAACTGGATCAGACTGTACTGGAG 1260
QY 1261 GAAAGCATTCAGAACTCCTATTCAACCTGGGCTCAAGGTTCTCAGGACAGTACCTGGAT 1320
Db 1261 GAAAGCATTCAGAACTCCTATTCAACCTGGGCTCAAGGTTCTCAGGACAGTACCTGGAT 1320
QY 1321 GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCAGTTCTCACCCCTGCTCC 1380
Db 1321 GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCAGTTCTCACCCCTGCTCC 1380
QY 1381 TGCTCAGCGTCCCAACAGGCACTGCACAGAAAGGCTGAGTGGAAAGTCCCACTGTCTATCTC 1440
Db 1381 TGCTCAGCGTCCCAACAGGCACTGCACAGAAAGGCTGAGTGGAAAGTCCCACTGTCTATCTC 1440
QY 1441 CTGGGTTTCTCTGCTCTTTTATTTTGGTGATCCTGGTCTTTCGGCCGTTTTCACGTCAATTG 1500
Db 1441 CTGGGTTTCTCTGCTCTTTTATTTTGGTGATCCTGGTCTTTCGGCCGTTTTCACGTCAATTG 1500

QY 1501 TGTGCACCTCAGCTGAAAGTTGCTGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGCAGGCT 1560
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1501 TGTGCACCTCAGCTGAAAGTTGCTGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGCAGGCT 1560
QY 1561 GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAAGTGTGGCAGTGCCC 1620
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1561 GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAAGTGTGGCAGTGCCC 1620
QY 1621 TGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCC 1680
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1621 TGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCC 1680
QY 1681 GACACAGGTGTTACATCTGTCTGTCTCAGGTGAGTGCCTCAGTTCCTTGGAAAGCTAGGT 1740
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1681 GACACAGGTGTTACATCTGTCTGTCTCAGGTGAGTGCCTCAGTTCCTTGGAAAGCTAGGT 1740
QY 1741 TCCTGCGACTGTTACCAAGGTGATTGTAAGAGCTGGCGGTACAGAGGAACAAGCCCC 1800
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1741 TCCTGCGACTGTTACCAAGGTGATTGTAAGAGCTGGCGGTACAGAGGAACAAGCCCC 1800
QY 1801 CAGCTGAGGGGGTGTGTAATCGGACAGCCTCCAGCAGAGGTGTGGAGCTGCAGCTGA 1860
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1801 CAGCTGAGGGGGTGTGTAATCGGACAGCCTCCAGCAGAGGTGTGGAGCTGCAGCTGA 1860
QY 1861 GGAAGAAGAGACAATCGGCTGGACACTCAGGAGGTCAAAAGGAGACTTGGTGGCACC 1920
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1861 GGAAGAAGAGACAATCGGCTGGACACTCAGGAGGTCAAAAGGAGACTTGGTGGCACC 1920
QY 1921 ACTCATCTGCCACCCCGAGATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGG 1980
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1921 ACTCATCTGCCACCCCGAGATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGG 1980
QY 1981 CGGACGTTTTCTGTTGGAAATCTTAGTCCTTGGCCTCGGACACCTTCATTCGTTAGCTGG 2040
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1981 CGGACGTTTTCTGTTGGAAATCTTAGTCCTTGGCCTCGGACACCTTCATTCGTTAGCTGG 2040
QY 2041 GGAGTGGTGGTGAGGAGTGAAGAAGAGCGGATGGTCACACTCAGATCCACAGAGCCCA 2100
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2041 GGAGTGGTGGTGAGGAGTGAAGAAGAGCGGATGGTCACACTCAGATCCACAGAGCCCA 2100
QY 2101 GGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCACCCCTGCAC 2160
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2101 GGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCACCCCTGCAC 2160
QY 2161 AGCCCTCATCCCTCTTGGCTTGAGCCGTGAGAGSCCTGTGTGAGTGTCTGACCCGAGA 2220
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2161 AGCCCTCATCCCTCTTGGCTTGAGCCGTGAGAGSCCTGTGTGAGTGTCTGACCCGAGA 2220
QY 2221 CACTCACAGCTTTGTCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTGCCACG 2280
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2221 CACTCACAGCTTTGTCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTGCCACG 2280
QY 2281 CTTGCACCTCGGGCCCATCTGGGCTCATGCTCTCTCCTGCTATTGAAATTAGTACCTAG 2340
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2281 CTTGCACCTCGGGCCCATCTGGGCTCATGCTCTCTCCTGCTATTGAAATTAGTACCTAG 2340
QY 2341 CTGCACACAGTATGTAGTTACCAAAGAATAACGGCAATAATTGAGAAAAAAA 2395
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2341 CTGCACACAGTATGTAGTTACCAAAGAATAACGGCAATAATTGAGAAAAAAA 2395

RESULT 14

ACD28828
ID ACD28828 standard; cDNA; 2395 BP.

XX
AC ACD28828;

XX
DT 27-AUG-2003 (first entry)

XX
DE Human secreted / transmembrane polypeptide PRO4405 cDNA.

XX
KW Human; ss; gene; gene therapy; diabetes; obesity; hypoinsulinaemia.

XX OS Homo sapiens.
XX
PN US2003027249-A1.
XX
PD 06-FEB-2003.
XX
PF 16-AUG-2001; 2001US-00931836.
XX
PR 15-MAY-1998; 98US-0085579P.
PR 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.
PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 12-JAN-1999; 99US-0115552P.
PR 22-JAN-1999; 99US-0116843P.
PR 23-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0131291P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132383P.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 25-AUG-1999; 99US-00380142.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99WO-US028551.
PR 22-DEC-1999; 99WO-US030720.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001US-00869599.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
XX
PA (GETH) GENENTECH INC.
XX
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-492030/46.
DR P-PSDB; ABO19428.
XX
PT New isolated, secreted and transmembrane PRO polypeptides and encoding
PT nucleic acids, useful for the diagnosis and treatment of disorders such

PT	as diabetes, obesity and/or hypoinsulinemia.
XX	Claim 1; Fig 19; 196pp; English.
PS	
XX	The invention relates to a new isolated nucleic acid which encodes a PRO
CC	polypeptide. The methods and compositions of the present invention are
CC	useful for the diagnosis and treatment of disorders associated with the
CC	PRO polypeptides, such as diabetes, obesity and hypoinsulinemia. The
CC	present sequence represents cDNA encoding a human secreted and
CC	transmembrane PRO polypeptide
XX	
SQ	Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;
	Query Match 100.0%; Score 2395; DB 7; Length 2395;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCTGGAGCGGGAAGCGGGCTGCAGAGGCGGAGGCTCCAGGTGGGTGGTTCGGCATC 60
Db	
QY	61 CAGCCTAGCGTGTCCACGATGCGGTGGCTCCGGGACTTTTCGCTACCTGTTGCGTAGCG 120
Db	
QY	61 CAGCCTAGCGTGTCCACGATGCGGTGGCTCCGGGACTTTTCGCTACCTGTTGCGTAGCG 120
QY	121 ATCGAGGTGCTAGGGATCGGGTCTTCTTCGGGGATTTCTCCGGGTCCCGTTCGTTCC 180
Db	
QY	121 ATCGAGGTGCTAGGGATCGGGTCTTCTTCGGGGATTTCTCCGGGTCCCGTTCGTTCC 180
QY	181 TCTGCCAGAGCGGAACACGGAGCGGAGCCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
Db	
QY	181 TCTGCCAGAGCGGAACACGGAGCGGAGCCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
QY	241 TCTAACTGGACCGCTGCCACCACTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGAT 300
Db	
QY	241 TCTAACTGGACCGCTGCCACCACTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGAT 300
QY	301 GCCTTGAGAGATGATTTGTGTTGGGTCAAGGGTGTGAAATTTATGCCCTACACAACT 360
Db	
QY	301 GCCTTGAGAGATGATTTGTGTTGGGTCAAGGGTGTGAAATTTATGCCCTACACAACT 360
QY	361 TACCTTGAGAGATGATTTGTGTTGGGTCAAGGGTGTGAAATTTATGCCCTACAGTT 420
Db	
QY	361 TACCTTGAGAGATGATTTGTGTTGGGTCAAGGGTGTGAAATTTATGCCCTACAGTT 420
QY	421 ACTATGCCCTCGAATCAAGGCATTTGATGACGGGAGCCTTCTGGCTTTGTCGAGCTCATC 480
Db	
QY	421 ACTATGCCCTCGAATCAAGGCATTTGATGACGGGAGCCTTCTGGCTTTGTCGAGCTCATC 480
QY	481 AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGCAAGCAAAAGCAGCT 540
Db	
QY	481 AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGCAAGCAAAAGCAGCT 540
QY	541 GGAAAAAGAAATAGTCTTTTATGGAGATGAAACCTGGGTTAAATTTATCCCAAAGCATTTT 600
Db	
QY	541 GGAAAAAGAAATAGTCTTTTATGGAGATGAAACCTGGGTTAAATTTATCCCAAAGCATTTT 600
QY	601 GTGGAATATGATGGAAACAACTCATTTTTCGTGTGAGATTACACAGAGGTGGATAATAAT 660
Db	
QY	601 GTGGAATATGATGGAAACAACTCATTTTTCGTGTGAGATTACACAGAGGTGGATAATAAT 660
QY	661 GTACAGAGGCATTTGGATAAGTATTAAAAAGAGGAGATTGGGACATATTAATCCTCCAC 720
Db	
QY	661 GTACAGAGGCATTTGGATAAGTATTAAAAAGAGGAGATTGGGACATATTAATCCTCCAC 720
QY	721 TACCTGGGCTGGACCAATTTGGCCACATTTTCAGGGCCCAACAGCCCCCTGATTGGGAG 780
Db	
QY	721 TACCTGGGCTGGACCAATTTGGCCACATTTTCAGGGCCCAACAGCCCCCTGATTGGGAG 780
QY	781 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACTCATCTGCAGTCGAAGGAG 840
Db	
QY	781 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACTCATCTGCAGTCGAAGGAG 840

QY	841 AGAGAGACGCCCTTTACCAATTTGCTGTTCTTTTGTGTGACCATGGCATGTCTGAAACA 900
Db	
QY	841 AGAGAGACGCCCTTTACCAATTTGCTGTTCTTTTGTGTGACCATGGCATGTCTGAAACA 900
QY	901 GGAAGTCACGGGGCCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT 960
Db	
QY	901 GGAAGTCACGGGGCCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT 960
QY	961 GCGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGACGTCCTCAATAGACGGATGTG 1020
Db	
QY	961 GCGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGACGTCCTCAATAGACGGATGTG 1020
QY	1021 GCTCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGAGCCTC 1080
Db	
QY	1021 GCTCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGAGCCTC 1080
QY	1081 CTATTTCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
Db	
QY	1081 CTATTTCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
QY	1141 ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCCGTCAATGAAAAAGATCCTGGG 1200
Db	
QY	1141 ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCCGTCAATGAAAAAGATCCTGGG 1200
QY	1201 TTTGAGCAGTTTAAAATGTGCAAGAGAATGTGGAAGTGGAACTGGATCAGACTGTACTTGGAG 1260
Db	
QY	1201 TTTGAGCAGTTTAAAATGTGCAAGAGAATGTGGAAGTGGAACTGGATCAGACTGTACTTGGAG 1260
QY	1261 GAAAGCATTGAGAAAGTCTTATTCACCTGGGCTCCAAGTTCTCAGGAGTACCTGGAT 1320
Db	
QY	1261 GAAAGCATTGAGAAAGTCTTATTCACCTGGGCTCCAAGTTCTCAGGAGTACCTGGAT 1320
QY	1321 GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCAGTTCTCACCTGCTCC 1380
Db	
QY	1321 GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCAGTTCTCACCTGCTCC 1380
QY	1381 TGCTCAGCGTCCACAGGCACCTGCACAGAAAGCTGAGCTGGAAGTCCCACTGTCTCATCTC 1440
Db	
QY	1381 TGCTCAGCGTCCACAGGCACCTGCACAGAAAGCTGAGCTGGAAGTCCCACTGTCTCATCTC 1440
QY	1441 CTGGGTTTCTCTGCTCTTTTATTTTGGTGATCTGTTCTTTTCGGCCGTTTTCACGTCTATTG 1500
Db	
QY	1441 CTGGGTTTCTCTGCTCTTTTATTTTGGTGATCTGTTCTTTTCGGCCGTTTTCACGTCTATTG 1500
QY	1501 TGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGCAGGCT 1560
Db	
QY	1501 TGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGCAGGCT 1560
QY	1561 GCCTTTTCGTTTACAGACTCTGTTTGAACACCTGGTGTGTCCTGAGTGTGAGTGTGCCCC 1620
Db	
QY	1561 GCCTTTTCGTTTACAGACTCTGTTTGAACACCTGGTGTGTCCTGAGTGTGAGTGTGCCCC 1620
QY	1621 TGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCTTATCCAGGCCTCTGGGTGTCTCC 1680
Db	
QY	1621 TGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCTTATCCAGGCCTCTGGGTGTCTCC 1680
QY	1681 GACACAGGTGTTTACATCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1740
Db	
QY	1681 GACACAGGTGTTTACATCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1740
QY	1741 TCCTGCGACTGTTTACCAAGGTGATTGTAAGAGCTGGCGGTGAGTGTGAGTGTGAGTGTGAGT 1800
Db	
QY	1741 TCCTGCGACTGTTTACCAAGGTGATTGTAAGAGCTGGCGGTGAGTGTGAGTGTGAGTGTGAGT 1800
QY	1801 CAGCTGAGGGGGTGTGTAATCGGACAGCCTCCAGCAGAGGTGTGGAGTGTGAGTGTGAGTGTGAGT 1860
Db	
QY	1801 CAGCTGAGGGGGTGTGTAATCGGACAGCCTCCAGCAGAGGTGTGGAGTGTGAGTGTGAGTGTGAGT 1860
QY	1861 GGAAGAAAGAGACAATCGGCTGGACACTCAGGAGGGTCAAAAGGAGACTTGGTGGCACC 1920
Db	
QY	1861 GGAAGAAAGAGACAATCGGCTGGACACTCAGGAGGGTCAAAAGGAGACTTGGTGGCACC 1920
QY	1921 ACTCATCTGCGCAACCCCAAGATGATCTCTGCCTCATCAGGTCCAGATTTCTTTCCAAAGG 1980

Db 1921 ACTCATCTGCCCACCCAGAAATGCATCTGCCTCATCAGGTCAGATTTCTTCCAAGG 1980
QY 1981 CGGACGTTTCTGTTGGAATCTTAGTCCTTGGCCTCGGACACCTTCATTCTGTTAGCTGG 2040
Db 1981 CGGACGTTTCTGTTGGAATCTTAGTCCTTGGCCTCGGACACCTTCATTCTGTTAGCTGG 2040
QY 2041 GGAGTGGTGGTGAGGCGAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCCA 2100
Db 2041 GGAGTGGTGGTGAGGCGAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCCA 2100
QY 2101 GGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTGGGCCCCCACCACCCCTGCAC 2160
Db 2101 GGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTGGGCCCCCACCACCCCTGCAC 2160
QY 2161 AGCCCTCATCCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGTCTGACCCGAGA 2220
Db 2161 AGCCCTCATCCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGTCTGACCCGAGA 2220
QY 2221 CACTCACAGCTTTGTGCATCAGGCGCACAGGCTTCTCGAGCCAGGATGATCTGTGCCACG 2280
Db 2221 CACTCACAGCTTTGTGCATCAGGCGCACAGGCTTCTCGAGCCAGGATGATCTGTGCCACG 2280
QY 2281 CTTGCACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG 2340
Db 2281 CTTGCACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG 2340
QY 2341 CTGCACACAGTATGATGTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA 2395
Db 2341 CTGCACACAGTATGATGTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA 2395

RESULT 15
ACA60432
ID ACA60432 standard; cDNA; 2395 BP.
XX
AC ACA60432;
XX
DT 11-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO4405 cDNA.
XX
KW Human; secreted and transmembrane polypeptide; gene;
KW ss. chromosome mapping; gene mapping; transgenic animal; knockout animal;
KW therapeutic agent screening; chromosome identification; tissue typing;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2003018183-A1.
XX
PD 23-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063512.
XX
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-330984/31.
DR P-PSDB; ABU72021.
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acid
PT molecules encoding the polypeptides, useful in gene therapy or preparing
PT a medicament for treating a condition that is responsive to the PRO
PT polypeptide or antibody.
XX
PS Disclosure; Fig 139; 409pp; English.
XX
CC The invention describes novel isolated PRO polypeptides. The PRO

CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide
XX
SQ Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;
Query Match 100.0%; Score 2395; DB 7; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGAGCCGGAAGCGCGCTGCAGCAGGCGGAGGCTCCAGGTGGGTTCGGTTCGCGCATC 60
Db 1 CCTGGAGCCGGAAGCGCGCTGCAGCAGGCGGAGGCTCCAGGTGGGTTCGGTTCGCGCATC 60
QY 61 CAGCCTAGCGTGTCCACGATCGCGCTGGGCTCCGGACTTTCGTAACCTGTTGGGTAGCG 120
Db 61 CAGCCTAGCGTGTCCACGATCGCGCTGGGCTCCGGACTTTCGTAACCTGTTGGGTAGCG 120
QY 121 ATCGAGGTGCTAGGGATCGCGGTCTTCCCTTCGGGGATCTTCCCGGCTCCCGTTCGTTCC 180
Db 121 ATCGAGGTGCTAGGGATCGCGGTCTTCCCTTCGGGGATCTTCCCGGCTCCCGTTCGTTCC 180
QY 181 TCTGCCAGAGCGGAAACACGAGCGGAGCCCCCAGGCCCCGAAACCTTCGGCTGGAGCCAGT 240
Db 181 TCTGCCAGAGCGGAAACACGAGCGGAGCCCCCAGGCCCCGAAACCTTCGGCTGGAGCCAGT 240
QY 241 TCTAACTGGACCAAGCTGCCACCATCTCTTTCAGTAAAGTTGTTATTGTTCTGATAGAT 300
Db 241 TCTAACTGGACCAAGCTGCCACCATCTCTTTCAGTAAAGTTGTTATTGTTCTGATAGAT 300
QY 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGTTGTGAAATTTATGCCCTACACAACT 360
Db 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGTTGTGAAATTTATGCCCTACACAACT 360
QY 361 TACCTTGTGGAAGGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAGCCACCTACAGTT 420
Db 361 TACCTTGTGGAAGGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAGCCACCTACAGTT 420
QY 421 ACTATGCCTCGAATCAAGGCATTGATGACGGGGAGCCCTTCTGGCTTTGTCGACGTCATC 480
Db 421 ACTATGCCTCGAATCAAGGCATTGATGACGGGGAGCCCTTCTGGCTTTGTCGACGTCATC 480
QY 481 AGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAGCAGCT 540
Db 481 AGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAGCAGCT 540
QY 541 GGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTTAAATTTATCCCAAAGCATTTT 600
Db 541 GGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTTAAATTTATCCCAAAGCATTTT 600
QY 601 GTGGAATATGATGGAACCAACCTCATTTTTCGTGTCAGATTACACAGAGTGGATAATAAT 660
Db 601 GTGGAATATGATGGAACCAACCTCATTTTTCGTGTCAGATTACACAGAGTGGATAATAAT 660
QY 661 GTCACGAGGCATTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTATCTCCAC 720
Db 661 GTCACGAGGCATTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTATCTCCAC 720
QY 721 TACCTGGGGCTGGACCAACATTGGCCACATTTCAGGGCCCCAACAGCCCCCTGATTGGGCAG 780
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Db			
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QY	901	GGAAGTCACGGGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT	960
Db			
QY	901	GGAAGTCACGGGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT	960
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QY	1261	GAAAAGCATTCAGAAAGTCTTATTCACACCTGGGCTCCAAGTTCTCAGGCAGTACCTGGAT	1320
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QY	1381	TGCTCAGCGTCCACAGGCACCTGCACAGAAAGCTGAGCTGGAAGTCCCACTGTCACTC	1440
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QY	1441	CTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTGGCCGTTACAGTCATTG	1500
Db			
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Search completed: August 5, 2004, 18:16:00
Job time : 1005 secs

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Db			
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Db			
QY	1921	ACTCATCTGCCACCCCAAGATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAAG	1980
Db			
QY	1981	CGGACGTTTCTGTTGGAATTTCTTAGTCCTTGGCCTCGGACACCTTCATTCGTTAGCTGG	2040
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QY	1981	CGGACGTTTCTGTTGGAATTTCTTAGTCCTTGGCCTCGGACACCTTCATTCGTTAGCTGG	2040
Db			
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Db			
QY	2101	GGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGSCCCCAACCCCTGCAC	2160
Db			
QY	2101	GGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGSCCCCAACCCCTGCAC	2160
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QY	2161	AGCCCTCATCCCTCTTGGCTTGAGCCCTCAGAGGCCCTGTGCTGAGTGTCTGACCCGAGA	2220
Db			
QY	2161	AGCCCTCATCCCTCTTGGCTTGAGCCCTCAGAGGCCCTGTGCTGAGTGTCTGACCCGAGA	2220
Db			
QY	2221	CACCTCAGCTTTGTTCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTGCCACG	2280
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QY	2341	CTGCACACAGTATGTAGTTACCAAAAAGAAATAAACGGCAATAATTGAGAAAAAAA	2395
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QY	2341	CTGCACACAGTATGTAGTTACCAAAAAGAAATAAACGGCAATAATTGAGAAAAAAA	2395
Db			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2004, 08:51:20 ; Search time 58 Seconds
(without alignments)
3.894 Million cell updates/sec

Title: US-10-036-150-44
Perfect score: 2395
Sequence: 1 cctggagccggaagcgccg.....gcaataattgagaaaaaaa 2395

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 60 seqs, 47150 residues
Total number of hits satisfying chosen parameters: 120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : rst44.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Query		Description	
Result No.	Score	Match	Length	ID	%			
C 1	405	16.9	418	1	AQ673215		ACCESSION: AQ673215	
2	395.2	16.5	434	1	BE549374		ACCESSION: BE549374	
C 3	390.4	16.3	1201	1	BX377107		ACCESSION: BX377107	
C 4	371.8	15.5	390	1	BX097186		ACCESSION: BX097186	
5	371.8	15.5	640	1	BU425116		ACCESSION: BU425116	
6	356.7	14.9	920	1	BG336024		ACCESSION: BG336024	
7	356.7	14.9	970	1	BG336399		ACCESSION: BG336399	
8	340.5	14.2	674	1	BG927822		ACCESSION: BG927822	
9	338	14.1	557	1	BE757899		ACCESSION: BE757899	
C 10	314.2	13.1	368	1	AW262524		ACCESSION: AW262524	
11	309.7	12.9	332	1	BM844459		ACCESSION: BM844459	
12	308.9	12.9	595	1	BG346870		ACCESSION: BG346870	
C 13	305.6	12.8	405	1	AW262485		ACCESSION: AW262485	
14	304	12.7	570	1	BE669243		ACCESSION: BE669243	
C 15	300.799	12.6	739	1	CA377408		ACCESSION: CA377408	
16	300.6	12.6	319	1	AA687924		ACCESSION: AA687924	
17	295.6	12.3	412	1	BM107678		ACCESSION: BM107678	
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19	287.2	12.0	508	1	CB783017		ACCESSION: CB783017	
C 20	281.3	11.7	631	1	AL871903		ACCESSION: AL871903	
21	263	11.0	510	1	CB548333		ACCESSION: CB548333	
C 22	248.4	10.4	418	1	CB765650		ACCESSION: CB765650	
23	237.9	9.9	253	1	AA361388		ACCESSION: AA361388	
24	229	9.6	976	1	CD516167		ACCESSION: CD516167	
25	217.4	9.1	253	1	T32542		ACCESSION: T32542	
C 26	211	8.8	1205	1	BF791461		ACCESSION: BF791461	
27	206.2	8.6	350	1	BQ293001		ACCESSION: BQ293001	
C 28	205	8.6	318	1	Z44206		ACCESSION: Z44206	
29	200	8.4	806	1	BG923173		ACCESSION: BG923173	
C 30	200	8.4	3150	1	BC051059		ACCESSION: BC051059	
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C 32	192.4	8.0	789	1	BG389289		ACCESSION: BG389289	
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C 34	184.5	7.7	318	1	BI051441	ACCESSION: BI051441
35	173.6	7.2	517	1	BI391754	ACCESSION: BI391754
C 36	172.6	7.2	355	1	BF746141	ACCESSION: BF746141
37	165.2	6.9	264	1	BI026475	ACCESSION: BI026475
C 38	163.4	6.8	764	1	BX077539	ACCESSION: BX077539
39	160.4	6.7	252	1	AA356939	ACCESSION: AA356939
C 40	158.2	6.6	744	1	BX077538	ACCESSION: BX077538
41	153.8	6.4	739	1	BUI30677	ACCESSION: BUI30677
42	123	5.1	758	1	BI080925	ACCESSION: BI080925
43	116.4	4.9	460	1	BF442617	ACCESSION: BF442617
C 44	114.6	4.8	510	1	AL913388	ACCESSION: AL913388
45	110.4	4.6	720	1	CE024824	ACCESSION: CE024824
C 46	108.4	4.5	934	1	BE897861	ACCESSION: BE897861
47	107.4	4.5	122	1	BQ360060	ACCESSION: BQ360060
C 48	106.8	4.5	556	1	BM323673	ACCESSION: BM323673
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C 50	103.1	4.3	990	1	BM468049	ACCESSION: BM468049
51	103.1	4.3	2495	1	BC036916	ACCESSION: BC036916
C 52	103.1	4.3	3270	1	AY408630	ACCESSION: AY408630
53	102.5	4.3	466	1	BZ270849	ACCESSION: BZ270849
C 54	99.4001	4.2	560	1	BJ434815	ACCESSION: BJ434815
55	96.6002	4.0	880	1	CD387014	ACCESSION: CD387014
C 56	96.2002	4.0	3270	1	AY408631	ACCESSION: AY408631
57	93.8002	3.9	545	1	AW862654	ACCESSION: AW862654
C 58	90.6002	3.8	3282	1	AY408632	ACCESSION: AY408632
59	89	3.7	124	1	BE685541	ACCESSION: BE685541
C 60	87.8	3.7	140	1	CD733602	ACCESSION: CD733602

ALIGNMENTS

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LOCUS
DEFINITION HS_5496_A2_G07_SP6E RPCI-11 Human Male DNA linear GSS 24-JUN-1999
Genomic clone Plate=1072 Col=14 Row=M, genomic survey sequence.
ACCESSION AQ673215
VERSION AQ673215.1 GI:5205961
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 418)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 1072 row: M column: 14
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 418.
Location/Qualifiers
1. .418
/organism="Homo sapiens"

FEATURES
source

/mol_type="genomic DNA"
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/clone="plate=1072 Col=14 Row=M"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites"

Query Match	16.9%;	Score 405;	DB 1;	Length 418;
Best Local Similarity	98.6%;	Pred. No. 0;		
Matches 408;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
QY	1589	CACCTGGTGTGTGCCAAGTCTGGCAGTGCCTTGACAGGGGGCTTCAGGGAAGACGTG	1648	
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QY	1649	GAGCAGCCTTATCCAGGCTCTGGGTGTCCCGACACAGGTGTTTACATCTGTGCTGTCA	1708	
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QY	1709	GGTCAGATGCCTCAGTCTTGGAAAGCTAGGTTCCCTGCACTGTTTACCAAGGTGATTGTA	1768	
Db	298	GGTCAGATGCCTCAGTCTTGGAAAGCTAGGTTCCCTGCACTGTTTACCAAGGTGATTGTA	239	
QY	1769	AAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAATCGACAG	1828	
Db	238	AAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAATCGACAG	179	
QY	1829	CCTCCAGCAGAGGTGTGGAGCTGCAGCTGAGGGAAGAGACAATCGGCCCTGGACAC	1888	
Db	178	CCTCCAGCAGAGGTGTGGAGCTGCAGCTGAGGGAAGAGACAATCGGCCCTGGACAC	119	
QY	1889	TCAGGAGGTCAAAAGGAGACTTGGTGCACCACTCATCTGCCACCCCCAGAAATGCATC	1948	
Db	118	TCAGGAGGTCAAAAGGAGACTTGGTGCACCACTCATCTGCCACCCCCAGAAATGCATC	59	
QY	1949	CTGCCTCATCAGGTCCAGATTCTTTTCCAAGCGGACGTTTCTGTTGGAATTC	2002	
Db	58	CTGCCTCATCAGGTCCAGATTCTTTTCCAAGCGGACGTTTCTGTTGGAATATC	5	

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BE549374
LOCUS
DEFINITION
BE549374 434 bp mRNA linear EST 09-AUG-2000
601074602F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460537 5',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 434)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM8455 row: c column: 02
High quality sequence stop: 432.
Location/Qualifiers
1. .434

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/clone="IMAGE:3460537"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

Query Match	16.5%;	Score 395.2;	DB 1;	Length 434;
Best Local Similarity	98.0%;	Pred. No. 0;		
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QY	1021	GCTGCGACACTGGCGATAGCACATTGGCTTACCAGTTCCTGATGAGAGAGCAGTGTAGGAGCCTC	1080	
Db	61	GCTGCGACACTGGCGATAGCACATTGGCTTACCAGTTCCTGATGAGAGAGCAGTGTAGGAGCCTC	120	
QY	1081	CTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT	1140	
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Db	181	ACGGGGCAGCTTAGTAAAGTGTGCAAGAGAAATGTCGCTCATATGAAAAAGATCCTGGG	240	
QY	1201	TTTGAGCAGTTTAAATGTCAGAAAGATTGCAATGGGAAGTGGATGAGACTGTACTTGGAG	1260	
Db	241	TTTGAGCAGTTTAAATGTCAGAAAGATTGCAATGGGAAGTGGATGAGACTGTACTTGGAG	300	
QY	1261	GAAAAGCATTGAGAGTCTTATTTCAACCTGGCTTCAAGGTTCTCAGGCAGTACCTGGAT	1320	
Db	301	GAAAAGCATTGAGAGTCTTATTTCAACCTGGCTTCAAGGTTCTCAGGCAGTACCTGGAT	360	
QY	1321	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCCCAGTTC	1368	
Db	361	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCCCAGTAC	408	

RESULT 3
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LOCUS
DEFINITION
BX377107 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI002YE24 3-PRIME, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2614.f For
more information about this cluster, see
<http://www.genoscope.cns.fr/>
cgi-bin/cluster.cgi?seq=CS0DI002BC12NP1&cluster=2614.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI002BC12NP1.

FEATURES
source

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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CS0DI002YE24"
/tissue_type="PLACENTA"
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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QY 174 TCGTTCCTCTGCCAGAGCGGAACACGAGCGGAGCCCCCAGCGCCCGAACCCCTCGGCTGG 233
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Db 299 CACAACCTTACCTTGTGGAAGGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACC 358
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QY 414 TACAGTTACTATGCCTCGAATCAAGG 439
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Db 359 TACAGTTACTATGCCTCGAATCAAGG 384
|||||

RESULT 7
BG336399
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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602405340F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4542968 5',
mRNA sequence.
BG336399
BG336399.1 GI:13142837
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 970)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCML223 row: p column: 09
High quality sequence stop: 661.
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/clone="IMAGE:4542968"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES
source

1..970
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4542968"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 14.9%; Score 356.7; DB 1; Length 970;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 380; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

QY 54 CCGCATCCAGCCTAGCGTGTCCACGATGCGGCTGGCTCCGGACTTTCGTTACCTGTTG 113
|||||

Db 2 CCGCATCCAGCCTAGCGTGTCCACGATCGGCTGGCTCCGGACTTTCGCTACCTGTTG 61
|||||
QY 114 CGTAGCGATCGAGTGTCTAGGATCGCGTCTTCTTCGGGGATTCTTCCCGGCTCCCGT 173
|||||
Db 62 CGTAGCGATCGAGTGTCTAGGATCGCGTCTTCTTCGGGGATTCTTCCCGGCTCCCGT 121
|||||
QY 174 TCGTTCCTCTGCCAGAGCGGAACACGAGCGGAGCCCCCAGCGCCCGAACCCCTCGGCTGG 233
|||||
Db 122 TCGTTCCTCTGCCAGAGCGGAACACGAGCGGAGCCCCCAGCGCCCGAACCCCTCGGCTGG 181
|||||
QY 234 AGCCAGTTCTAACTGGACCACGCTGCCACACCTCTCTTTCAGTAAAGTTGTTTCT 293
|||||
Db 182 AGCCAGTTCTAACTGGACCACGCTGCCACACCTCTCTTTCAGTAAAGTTGTTTCT 241
|||||
QY 294 GATAGATGCCTTGAGAGATGATTTTGTGTTGGTCAAAGGGTGTGAATTTATGCCCTA 353
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Db 242 GATAGATGCCTTGAGAGATGATTTTGTGTTGGTCAAAGGGTGTGAATTTATGCCCTA 299
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QY 354 CACAACCTTACCTTGTGGAAGGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACC 413
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Db 300 CACAACCTTACCTTGTGGAAGGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACC 358
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QY 414 TACAGTTACTATGCCTCGAATCAAGG 439
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Db 359 TACAGTTACTATGCCTCGAATCAAGG 384
|||||

RESULT 8
BG927822
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
FEATURES
source

BG927822 674 bp mRNA linear EST 06-NOV-2001
HNC7-1-B4.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
BG927822
BG927822.1 GI:14322345
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 674)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
21482651
11597177
Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7.
Location/Qualifiers
1..674
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"

Query Match 14.2%; Score 340.5; DB 1; Length 674;
Best Local Similarity 72.5%; Pred. No. 0;
Matches 434; Conservative 0; Mismatches 10; Indels 155; Gaps 1;

QY 1352 CACAAGTGCCCGAGTTCTCACCCCTGCTCAGCGTCCACAGGCACTGCACAGAAA 1411
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Db	76	CACGCGTCCGCCAGTTCTCACCCCTGCTCCTGCTCAGCGTCCACAGGCACTGGCAGAA	135
QY	1412	GGCTGAGCTGGAAGTCCCACTGTCACTCCTCGGTTTCTCTGCTCTTTTATTGGTGAT	1471
Db	136	GGCTGAGCTGGAAGTCCCACTGTCACTCCTCGGTTTCTCTGCTCTTTTATTGGTGAT	195
QY	1472	CCTGGTCTTTCCGCCGTTACAGTCACTGTTGTGACCTCAGCTGAAAGTTCGTCTACTT	1531
Db	196	CCTGGTCTTTCCGCCGTTACAGTCACTGTTGTGACCTCAGCTGAAAGTTCGTCTACTT	255
QY	1532	CTGTGGCCTCTCGTGGCTGGCGG-----	1554
Db	256	CTGTGGCCTCTCGTGGCTGGCGGCAGGTGGGTGATGCTGGCTGGCCTCGGCGTGTGTG	315
QY	1555	-----	1554
Db	316	TGTGATTGTGTCTGTTCTGACCAACGTGCTCGTGGTGGAAACACCCCAAGGATGACG	375
QY	1555	-----	CA 1556
Db	376	TACGGCTGGTTCCTGGGAGTGTGACGTAGTCTTCTGCTCAGGTTGTTCTTGTATTCA	435
QY	1557	GGCTGCCCTTTCGTTTACCAGACTCTGGTTGAACACCTGGGTGTGCCAAGTCTGGCAGT	1616
Db	436	GGCTGCCCTTTCGTTTACCAGACTCTGGTTGAACACCTGGGTGTGCCAAGTCTGGCAGT	495
QY	1617	GCCTGGACAGGGGGCCTCAGGAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTG	1676
Db	496	GCCTGGACAGGGGGCCTCAGGAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTG	555
QY	1677	TCCGACACAGGTGTTACATCTGTGCTGTCAGGTCAGATGCCTCAGTCTTGGAAAGCT	1736
Db	556	TCCGACACAGGTGTTACATCTGTGCTGTCAGGTCAGATGCCTCAGTCTTGGAAAGCT	615
QY	1737	AGGTTCTCGCACTGTTTACCAGGTGATTTAAAGAGCTGGCGTCAAGAGGAACAAG	1795
Db	616	AGGTTCTCGCACTGTTTACCAGGTGATTTAAAGAGCTGGCGTCAAGAGGAACAAG	674
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BE757899			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PubMed			
COMMENT			
USDA, ARS, US Meat Animal Research Center			
PO Box 166, Clay Center, NE 68933-0166, USA			
Tel: 402 762 4366			
Fax: 402 762 4390			
Email: smith@email.marc.usda.gov			
Single pass sequencing. Bases called and alt trimmed with phred			
v0.980904.e. Vector identified by cross_match with the -minscore 18			
and -minmatch 12 options.			
PCR Primers			
FORWARD: AGGAAACAGCTATGACCAT			
BACKWARD: GTTTCCAGTCACGACG			
Plate: 65 row: K column: 17			
Seq primer: ATTAGGTGACACTATAG.			
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/mol_type="mRNA"			
/db_xref="taxon:9913"			
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/lab_host="DH10B"			
/clone lib="MARC 2BOV"			
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;			
Library made from pooled tissue from testis, thymus,			
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adrenal, and endometrium."			
Query Match			
Best Local Similarity			
Matches			
Score			
DB			
Length			
557;			
Pred. No. 0;			
Mismatches			
50;			
Indels			
6;			
Gaps			
1;			
QY	62	AGCCTAGCGTGTCCACGATCGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGA	121
Db	126	ACGCGAGGTGGGACACGATCGGCTCGGCTCCGGGACTTTCGCTCCGGCTGCGTCTGTA	185
QY	122	TCGAGGTGCTAGGATCGCGTCTTCTTCCGCGGATTTTCCCGGCTCCCGTTTCGTTCTT	181
Db	186	TCGAGGTCTCGGCTCGGCTGTTCTTCCGCGGCTTCTTCCCGGCTCCCGT-----CT	239
QY	182	CTGCCAGAGCGGAACACGAGCGGAGCCGCCAGCGCCGAAACCCCTCGGCTGGAGCCAGTT	241
Db	240	TTTCCGAGCGGAGCGGCAAGAGTCCCGGCGCCGAAACCCCTCTGCTGGAGCCAGTT	299
QY	242	CTAACTGGACCACTGCCACACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATG	301
Db	300	CCAACTGGACCGAGCTTCCACCAACCGCTCTTTCAGTAAAGTTGTTATTGTTCTGATAGATG	359
QY	302	CCTTGAGAGATGATTTTGTGTTGGTCAAAGGGTGTGAATTTATGCCCTACACAACTT	361
Db	360	CCTTGAGAGATGATTTTGTGTTGGATCAAAGGGTGTGAATTTATGCCCTACACAACTT	419
QY	362	ACCTGTGGAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACCTACAGTTA	421
Db	420	ATCTGTGGAAGGAGCATCTCTCAGTTTGTGGCTGAAGCAAGCCACCTACAGTTA	479
QY	422	CTATGCTCGAATCAAGGATGATGACGGGAGCCCTTCCGCTTGTTCGACGTCATCA	481
Db	480	CTATGCTCGAATCAAGGCGTTGCTGACAGGAGCCCTCCCTGGCTTCATCGATGTCGTC	539
QY	482	GGAACTCAATTCTCTCT 498	
Db	540	GGAACTCAATTCTCTCT 556	
RESULT 10			
AW262524/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
Unpublished (1998)			
AW262524			
xq85f10.x1 NCI CGAP Brn53 Homo sapiens cDNA clone			
similar to SW:YA93_SCHPO Q09782 HYPOTHETICAL 85.7 KD PROTEIN			
C13G6.03 IN CHROMOSOME 1.; mRNA sequence.			
AW262524			
AW262524.1 GI:6639340			
EST.			
Homo sapiens (human)			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
1 (bases 1 to 368)			
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
National Cancer Institute / National Institute of Neurological			
Disorders and Stroke, Brain Tumor Genome Anatomy Project			
(CGAP/BTGA), Tumor Gene Index			
Unpublished (1998)			
368 bp			
mRNA			
linear			
EST 28-DEC-1999			
IMAGE:2757451.3			

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 368.
Location/Qualifiers
1. .368
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2757451"
/tissue_type="three pooled meningiomas"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Brn53"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."

FEATURES

source
1. .368
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="NCI_CGAP Brn53"
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Query Match 13.1%; Score 314.2; DB 1; Length 368;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 358; Conservative 0; Mismatches 3; Indels 4; Gaps 4;

QY 323 TTGGTCAAAGGGTGTGAAATTATGCGCTACACAACCTTACCTTGTGGAAAAGGAGCAT 382
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Db 362 TTGGTCAAAGGGTGT-AAATTATGCCCTACACAACCTTCACTGTGG-AAAAGGAGCAT 305

QY 383 CTCACAGTTTGTGGCTGAAGCAAAAGCCACCTACA-GTTACTATGCCTCGAATCAAGGCA 441
|||||
Db 304 CTCACAGTTTG-GGCTGAAGCAAAAGCCACCTACAGGTTACTATGCCTCGAATCAAGGCA 246

QY 442 TTGATGACGGGGAGCCTTCCTGGCTTTGTGCGACGTCATCAGAAACCTCAATTCTCCTGCA 501
|||||
Db 245 TTGATGACGGGGAGCCTTCCTGGCTTTGTGCGACGTCATCAGAAACCTCAATTCTCCTGCA 186

QY 502 CTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCTGGAAAAAGAAATAGCTTTTAT 561
|||||
Db 185 CTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCTGGAAAAAGAAATAGCTTTTAT 126

QY 562 GGAGATGAACCTGGGTTAAATTATTTCCAAAGCATTTTGTGGAATATGATGGAACAACC 621
|||||
Db 125 GGAGATGAACCTGGGTTAAATTATTTCCAAAGCATTTTGTGGAATATGATGGAACAACC 66

QY 622 TCATTTTTCGTGTGATACAGAGGTGGATAATAATGTACGAGGCATTTGGATAAA 681
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Db 65 TCATTTTTCGTGTGATACAGAGGTGGATAATAATGTACGAGGCATTTGGATAAA 6

QY 682 GTATT 686
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Db 5 GTATT 1

RESULT 11

BM844459
LOCUS K-EST0122574 S13KMS5 Homo sapiens cDNA clone S13KMS5-36-B11 5',
DEFINITION mRNA sequence.

BM844459

BM844459.1 GI:19200858

EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 332)

REFERENCE

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

TITLE
JOURNAL
COMMENT

Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 36 row: B column: 11
High quality sequence stop: 332.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-36-B11"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
(A)+ RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then decapped with tobacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dT-selected mRNA by priming with
dT-tailed vector. The dT-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F' by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."

FEATURES

source
1. .332
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="S13KMS5-36-B11"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
(A)+ RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then decapped with tobacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dT-selected mRNA by priming with
dT-tailed vector. The dT-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F' by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."

Query Match 12.9%; Score 309.7; DB 1; Length 332;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 322; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1555 CAGGCTGCCTTTCGTTTACAGACTCTGGTTGAACACCTGGTGTGCCAAGTGTGGCA 1614
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QY 1615 GTGCCCTGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTTGGG 1674
|||||
Db 67 GTGCCCTGGACAGGTGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTTGGG 126

QY 1675 TGTCCCGACACAGGTGTTACATCTGTGCTGTCAAGTCAGATGCCTCAGTTCTTGGAAAG 1734
|||||
Db 127 TGTCCCGACACAGGTGTTACATCTGTGCTGTCAAGTCAGATGCCTCAGTTCTTGGAAAG 186

QY 1735 CTAGGTTCCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAA 1794
|||||
Db 187 CTAGGTTCCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAA 246

QY 1795 GCCCCCCAGCTGAGGGGGTGTGTGAATCGACAGCCTCCCAGCAGAGGTGTGGGAGCTGC 1854
|||||
Db 247 GCCCCCCCGCTGAGGGGGTGTGTGAATCGACAGCCTCCCAGCAGAGGTGTGGGAGCTGC 306

QY 1855 AGCTGAGGGAAGAAGAGACAATCGGC 1880
|||||
Db 307 AGCTGAGGGAAGAAGAGACAATCGGC 332

RESULT 12

BG346870

LOCUS

DEFINITION

BG346870 595 bp mRNA linear EST 28-FEB-2001
dad16g02.y1 Wellcome CRC PCS107 tropicalis St10-12 Silurana
tropicalis cDNA clone IMAGE:4439978 5' similar to SW:YA93_SCHPO

Q09782 HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I. ; ,
mRNA sequence.
BG346870
BG346870.1 GI:13167294
EST.
Silurana tropicalis (western clawed frog)
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 595)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L.,
Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y.,
Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
WashU Xenopus EST project, 1999
Unpublished (1999)
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by A. Zorn and J. Mason (Wellcome/CRC
Institute). DNA Sequencing by: Washington University Genome
Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 492.
Location/Qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:4439978"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="Wellcome CRC PCS107 tropicalis St10-12"
/note="Vector: PCS107; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Average
insert size 1.5 kb, range 0.5-4 kb. Library constructed by
A. Zorn and J. Mason (Wellcome/CRC Institute)."
Query Match 12.9%; Score 308.9; DB 1; Length 595;
Best Local Similarity 72.5%; Pred. No. 0;
Matches 413; Conservative 0; Mismatches 156; Indels 1; Gaps 1;
QY 248 GGACCACGTCGCCACCCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGA 307
DB 6 GGACAAAACCTTCCTTCACCTCTTTTCAAAAAGTTGTGCGTCCTTCATCGATGCTTTGA 65
QY 308 GAGATGATTTGTTGTTGGTCAAAGGGTGTGAAATTTATGCCCTACACAACTTACCTTG 367
DB 66 GACAGGACTTTGTGTATGTTCCAAAGGGGGAACATATATGCTTACCTTACCCAACTTG 125
QY 368 TGGAAAAAGGAGCATCTCACAGTTTGTGGTGAAGCAAAAGCCACCTACAGTTACTATGC 427
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QY 428 CTCGAATCAAGGCATTGATGACGGGAGCCTTCCTGGCTTTGTGACGTGATCAGGAACC 487
DB 186 CTCGTATCAAGGCCCTGATGACAGGTAGCATCCCTGGATTATTGATGTTGTAATGAATC 245
QY 488 TCAATTCTCCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCTGGAAAAA 547
DB 246 TAAATTACACGAATTACTGGATGACAAATGTGATATGCAAGGAAGCAAGCTGGAAAAA 305
QY 548 GAATAGTCTTTTATGGAGATGA-AACCTGGGTTAAATATTCCCAAAGCATTTTGTGGAA 606
DB 306 GGATAGTATTTTATGGAGATGATAACTTGGATAAAACTTTTCCCCAAACATTTTGTGAA 365

QY 607 TATGATGGAACAACCTCATTTTTTCGTGTCAGATTACACAGAGGTGGATAATAATGTACG 666
DB 366 TATGATGGAACAACATCATTTTTTGTCTGATTATACAGAGGTGATAATAATGTTACA 425
QY 667 AGGCATTTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAAATCCTCCACTACCTG 726
DB 426 AGGCATTTGATGATATATTAAAGAGAAATGACTGGGATATGCTTATCCTTCACTATCTT 485
QY 727 GGGCTGGACCATTTGGCCACATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAAGAGCTG 786
DB 486 GGATTAGATCACAATAGGACATTTAACAGGACCACATAGTCATTTAATCGTCCAAAACCTT 545
QY 787 AGCGAGATGGACAGCGTCTGATGAAGATC 816
DB 546 CTTGAATGGACACTGTCTCTAAAAAAATC 575
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AW262485/c
LOCUS
DEFINITION
AW262485
xq85a11.x1 NCI CGAP Brn53 Homo sapiens cDNA clone IMAGE:2757404 3'
similar to SW:YA93_SCHPO Q09782 HYPOTHETICAL 85.7 KD PROTEIN
C13G6.03 IN CHROMOSOME I. ; , mRNA sequence.
AW262485
AW262485.1 GI:6639301
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 405)
REFERENCE
AUTHORS
TITLE
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGA), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 255.
Location/Qualifiers
FEATURES
source
1..405
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2757404"
/tissue_type="three pooled meningiomas"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Brn53"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
Query Match 12.8%; Score 305.6; DB 1; Length 405;
Best Local Similarity 91.0%; Pred. No. 0;
Matches 355; Conservative 0; Mismatches 31; Indels 4; Gaps 3;
QY 301 GCCTTGAGAGATGATTTTGTGTTGGTCAAAGGGTGTGAAATTTATGCCCTACACA-AC 359
DB 390 GCCTTGAGAGATGATTTTGTGTTGGTCAAGGGTGTGAAATTTAATGCCCTACACANAC 331
QY 360 TTACCTTTGTGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAAGCCACTAC--A 417
DB 330 TTTACCTGGTGAAGGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAAGCCACTACCAG 271

RESULT 19
CB783017 508 bp mRNA linear EST 16-MAY-2003
LOCUS AMGNNUC:NRHY7-00049-E6-A nrhy7 (10850) Rattus norvegicus cDNA clone
DEFINITION nrhy7-00049-e6 5', mRNA sequence.
ACCESSION CB783017 GI:29871408
VERSION CB783017.1
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 508)
AUTHORS Angen EST Program.
TITLE Angen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00049 row: e column: 6.
Location/Qualifiers
1..508
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrhy7-00049-e6"
/clone_lib="nrhy7 (10850)"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; W Rat
hypothalamus adult female Wistar rat avg. insert size 2.3
kb fraction 6 and 7"

Query Match 12.0%; Score 287.2; DB 1; Length 508;
Best Local Similarity 73.6%; Pred. No. 0;
Matches 373; Conservative 0; Mismatches 88; Indels 46; Gaps 1;

QY 1036 ATAGCACTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTG 1095
Db 2 ATAGGACTCGGTTTGCCAATTCCCTAAAGATAATGTAGGAAGCCTCTATTCCCAGTTATA 61

QY 1096 GAAGGAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGT 1155
Db 62 GAGGGAAACAGATGAGAGAGCAGCTGAGATTTTACATTTTAAACACATTACAGCTTAGC 121

QY 1156 AAACGTGTTGCAAGAGAATGTGCCGTGTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAA 1215
Db 122 AAACATTGCAAGAAACATACCAGCCTATGAAAAAGATCCTGGATTGTAGCAGTTTAA 181

QY 1216 ATGTCAGAAAGATTGCATGGAACTGGATCAGACTGTACTTGGAGGAAAGCATTTCAGAA 1275
Db 182 ATGGCAGAAAGGTTGCATGGAACTGGGTCAAACCTGCTGGAAGAAACCATTCAGAC 241

QY 1276 GTCCTATTCAACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTG 1335
Db 242 ATTCTGCTTGGCTTGGGGACCAAAGTACTCAGGCAGTACCTGGGTGCCCTGAAGACCTG 301

QY 1336 AGCTTGTCCTGAGTGCCACAAGTGGCCCA----- 1364
Db 302 AGTCAGTCCCTGAGCACACAAGTGGCTCACTATGACATCTACTCAATGGCAGTGGGACA 361

QY 1365 -----GTTCTCACCTGCTCCTGCTCAGCGTCCACAGGCAGCTGCACAGA 1409
Db 362 CTCATGGTTTTGGAGGTTCTCACCTGTTTCTCCTTAGCACTCCACATGTGCTGTCAGA 421

QY 1410 AAGGCTGAGCTGGAAGTCCCACTGTCTATCTCCTGGGTTTCTCTGCTCTTTTATTGGTG 1469
Db 422 AAGGCTGAAGTGGATGTTCCCTGTTGTCTCCTGTTGTTCTCTGTTTCTGTTTACTGATA 481

QY 1470 ATCCTGGTTCTTTTCGGCCGTTTCACGTC 1496
Db 482 TTTTGGTTCTTTTCGGCCCATTCATGTC 508

RESULT 20
AL871903 631 bp mRNA linear EST 03-DEC-2003
LOCUS AL871903 XGC-egg Silurana tropicalis cDNA clone TEgg106m03 5', mRNA
DEFINITION sequence.
ACCESSION AL871903 GI:38661448
VERSION AL871903
KEYWORDS EST.
SOURCE Silurana tropicalis (western clawed frog)
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 631)
AUTHORS Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)
COMMENT On Sep 15, 2002 this sequence version replaced gi:22892168.
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TEgg106m03.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dt primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli XLI-blue.
Location/Qualifiers
1..631
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TEgg106m03"
/dev_stage="egg"
/lab_host="Escherichia coli XLI-blue"
/clone_lib="XGC-egg"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"

Query Match 11.7%; Score 281.3; DB 1; Length 631;
Best Local Similarity 67.0%; Pred. No. 0;
Matches 413; Conservative 0; Mismatches 202; Indels 1; Gaps 1;

QY 101 TCGCTACCTGTTGCGTAGCGATCGAGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCT 160
Db 16 TGGCATCTTGCTGCCTGTTAATCCAGGTCTTTGGAGCGATGCTTATTATCCGTGGCTTCT 75

QY 161 TCCCGGCTCCGTTTCGTTTC-CTCTGCCAGAGCGGAACACGAGCGGAGGCCCGCCAGCGCCC 219
Db 76 TTCTTTTACCGGTGGGTCTCAGTCACGGAAGAGCACCGAGCGCAGACCCACACAGAG 135

QY 220 GAACCCCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCCACCACCTCTCTTCAGTAAA 279
Db 136 CCAGCGACAGCAGGCTTACTCTCGAACTGGACAAAACCTTCCTTCACCTCTTTCAAAAA 195

QY 280 GTTGTTATTGTTCTGATAGATGCCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGGTGTG 339
Db 196 GTTGTGTCGTCATCTAATCGATGCTTTGAGACAGGACTTTGTGTATGGACGAGGGGAAG 255

QY 340 AAATTTTATGCCCTACACAACTTACCTTGIGGAAAGAGGATCTCACAGTTTGTGGCT 399
Db 256 AAACGTATGCCCTTACCATACCCAACTTGTAATAAAGGAACAAACACAGCTACATATCA 315

QY 400 GAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGAGCCTT 459

QY 1289 TGGGCTCCAAGGTTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGA 1348
Db 10 TCGGATCAAGGTTCTCAGGCAGTACTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGA 69
QY 1349 GTGCACAAGTGGCCCA----- 1364
Db 70 GTGCACAAGTGGCCCAAGTACGACATCTATTTCGATGATGGTGGGACTGTCGTGTTTTGG 129
QY 1365 --GTTCTCACCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGG 1422
Db 130 AGGTTCTCACCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGG 189
QY 1423 AAGTCCCACTGTCACTCTCCGGGTTTCTCTGCTCTTTTATTGGTGATCCTGGTCTTT 1482
Db 190 AAGTCCCACTGTCACTCTCTGGGTTTCTCTGCTCTTTTATTGGTGATCCTGGTCTTT 249
QY 1483 CGGCCGTTACGTCATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCT 1542
Db 250 CGGCCGTTACGTCATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCT 309
QY 1543 CGTGGCTGGCGGCAGG 1558
Db 310 CGTGGCTGGCGGCAGG 325
RESULT 25
T32542
LOCUS
DEFINITION
EST50552 Human Gall bladder Homo sapiens cDNA 5' end similar to
None, mRNA sequence.
T32542
T32542.1 GI:614640
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 253)
ADAMS,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,
Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., HinkleJr,P.S.,
Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,
Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,
Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,
Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,
Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
Nature 377, 3-174 (1995)
96026280
PUBMED
7566098
Other_ESTs: THC15950
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@db.tigr.org)
Seq primer: M13 Reverse.
Location/Qualifiers

source 1. .253
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):103110"
/db_xref="taxon:9606"
/clone_lib="Human Gall bladder"
/note="Organ: gallbladder"
Query Match 9.1%; Score 217.4; DB 1; Length 253;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 242; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
QY 11 GAAAGCGGGCTGCAGCAGGGCGAGGCTCCAGGTGGGTCGGTTCGGCATCCAGCCTAGCG 70
Db 2 GGAAGCGGGCTGCAGCAGGGCGAGGCTCCAGGTGGGTCGGTTCGGCATCCAGCCTAGCG 61
QY 71 TGTCCACGATCGGCTGGGCTCCGGGACTTTCGCTACCTGTTCGCTAGCGATCGAGGTGC 130
Db 62 TGTCCGCNATCGGCTGGGCTCCGGGACTTTCGCTACCTGTTCGCTAGCGATCGAGGTGC 120
QY 131 TAGGGATCGGGTCTTCTTCGGGGATTCTCCGGGCTCCGTTCCCTCTCTGCTCCAGAG 190
Db 121 TAGGGATCGGGTCTTCTTCGGGGATTCTTCGGGCTCCCGTTCCCTCTCTGCTCCAGAG 180
QY 191 CGGAACACGGAGCGGAGCCCCCAGCGCCGAAACCTCGGCTGGAGCCAGTCTAACTGGA 250
Db 181 CGGAACACGGAGCGGA-CCCCAGCGCCGAAACNTCGGNTGGAGCCATTCTAACTGGA 239
QY 251 CCACGCTGCCACCA 264
Db 240 CCACGTTGCCACCA 253
RESULT 26
BF791461
LOCUS
DEFINITION
BF791461 1205 bp mRNA linear EST 12-JAN-2001
602251501F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4343713 5',
mRNA sequence.
BF791461
BF791461.1 GI:12096515
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1205)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9961 row: b column: 02
High quality sequence stop: 328.
Location/Qualifiers
1. .1205
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4343713"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 84"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site 1:
NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.

/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="AN0094"
/note="Organ: amnion normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning_products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

Query Match 8.6%; Score 206.2; DB 1; Length 350;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 208; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 985 ATCCGACATCCAAAGCACGTCCAATAGAGGATGGCTGCGACACTGGCGATAGCACTT 1044
Db |||||||
QY 350 ATCCGACATCCAAAGCACGTCCAACAGACGATGTGGCTGCGACACTGGCGATAGCACTT 291
Db |||||||
QY 1045 GGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCTCTATTCCCAGTTGTGGAAGGAAGA 1104
Db |||||||
QY 290 GGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCTCTATTCCCAGTTGTGGAAGGAAGA 231
Db |||||||
QY 1105 CCAATGAGAGAGCAGTTGAGATTTTACATTTTGAATACAGTGCAGCTTAGTAACTGTTG 1164
Db |||||||
QY 230 CCAATGAGAGAGCAGTTGAGATTTTGTACATTTTGAATACAGTGCAGCTTAGTAACTGTTG 171
Db |||||||
QY 1165 CAAGAGAATGTGCCGTCATATGAAAAGATC 1195
Db |||||||
QY 170 CAAGAGAATGTGCCGTCATATGAAAAGGTC 140
Db |||||||

RESULT 28
Z44206 318 bp mRNA linear EST 14-NOV-1994
LOCUS HSC1VA011 normalized infant brain cDNA Homo sapiens cDNA clone
DEFINITION c-1va01, mRNA sequence.
ACCESSION Z44206
VERSION Z44206.1 GI:573331
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 318)
AUTHORS Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houligatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
JOURNAL 95277534
MEDLINE 7757816
PUBMED
COMMENT Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress library idt: C; Genexpress_sequence_idt: y1c-1va01
Seq primer: (-21)M13 universal.
Location/Qualifiers
1. .318
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="C-1va01"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"

Note: this is a NIH_MGC Library."

Query Match 8.8%; Score 211; DB 1; Length 1205;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 308; Conservative 0; Mismatches 35; Indels 12; Gaps 7;

QY 783 GCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACC-TCACTGAGTCTGAAGGAGA 841
Db |||||||
QY 842 GAGAGACGCTTTACCCAAATTTGCTGGTCTTGTGGTGACCATGGCATGTCTGAAACAG 901
Db |||||||
QY 61 GAGAGACGCTTTACCCAAATTTGCTGGTCTTGTGGTGACCATGGCATGTCTGAAACAG 120
Db |||||||
QY 902 GAAGTCACGGGGCTCC-TCCACCGAGGAGGTGAATACA-----CCTCTGATTTTAATCAG 956
Db |||||||
QY 121 GAAGTCACGGGGCTCCATCCACCGAGGAGGTGAATACAGCCTCTGATTATTAAATCAGAT 180
Db |||||||
QY 957 TTCTGCGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGCACG-TCCAATAGACGG 1015
Db |||||||
QY 181 TACTGCGTTGGAAGGAAACCCGGTGATATCCGACATCCAAAGCACGATCCAAACAGACGG 240
Db |||||||
QY 1016 ATGTGGC---TGCGACACTGGCGATAGCACTTGGCTTACCGA-TTCCAAAAGACAGTGTA 1071
Db |||||||
QY 241 ATGTGGCATGCGACACATGGACGATAGCACTTGGATTACCGAGTTCCAAAAGACAGTGTA 300
Db |||||||
QY 1072 GGGAGC-CTCCTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGA 1125
Db |||||||
QY 301 GGGAGCACTCTATTCCCAGTTGTGGAAGGCAAGACCACTGAGCAGAGCAGAAA 355
Db |||||||

RESULT 27
BQ293001/c 350 bp mRNA linear EST 15-MAY-2002
LOCUS PM1-AN0094-240800-002-d02 AN0094 Homo sapiens cDNA, mRNA sequence.
DEFINITION BQ293001
ACCESSION BQ293001
VERSION BQ293001.1 GI:20801951
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 350)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL 20202663
MEDLINE 10737800
PUBMED
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-AN0094-
240800-002-d02&t3=2000-08-24&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 350.
Location/Qualifiers
1. .350
/organism="Homo sapiens"
/mol_type="mRNA"

/clone_lib="normalized infant brain cdna"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev stage=3 months_old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soaress, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"

Query Match	8.6%;	Score 205;	DB 1;	Length 318;
Best Local Similarity	98.3%;	Pred. No. 0;		
Matches	226;	Conservative	0;	Mismatches 2;
				Indels 2;
				Gaps 2;
QY	4	GGAGCCGGAAGCGCGCTGCAGCAGGCGAGGCTCCAGGTGGGTCCGGTCCGCATCCAG	63	
Db	1	GGAGCCGGAAGCGCGCTGCAGCAGGCGAGGCTCCAGGTGGGTCCGCATCCAG	60	
QY	64	CCTAGCGTGTCACGATCGGCTGGGCTCCGGACTTTCGCTACCTGTGGTAGCGATC	123	
Db	61	CCTAGCGTGTCACGATCGGCTGGGCTCCGGACTTTCGCTACCTGTGGTAG-GATC	119	
QY	124	GAGTGCTAGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCTCT	183	
Db	120	GAGTGCTAGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGNTCCCGTTCGTTCTCT	179	
QY	184	GCCAGAGCGGAACACGGAGCGGAGCCCGCAGCGCCGAAACCTCGGCTGG	233	
Db	180	GCCAGAGCGGAACACGGAGCGGA-NCCCCAGCGCCCGAAACCTCGGCTGG	228	

RESULT 29	BG923173	806 bp	mRNA	linear	EST 05-JUN-2001
LOCUS	602824014F1 NCI_CGAP_Mam6	Mus musculus	cdna	clone	IMAGE:4952955 5',
DEFINITION	mRNA sequence.				
ACCESSION	BG923173				
VERSION	EST.				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 806)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov				

FEATURES	source
1..806	
/organism="Mus musculus"	
/mol_type="mRNA"	
/strain="FVB/N"	
/db_xref="taxon:10090"	
/clone="IMAGE:4952955"	
/sex="female, virgin"	
/tissue_type="infiltrating ductal carcinoma"	
/dev_stage="5 months"	
/lab_host="DH10B"	
/clone_lib="NCI_CGAP Mam6"	
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator	

Query Match	8.4%;	Score 200;	DB 1;	Length 806;
Best Local Similarity	71.0%;	Pred. No. 0;		
Matches	272;	Conservative	0;	Mismatches 65;
				Indels 46;
				Gaps 1;
QY	1222	GAAAGATTGCATGGGAACCTGGATCAGACTGTACTTTGGAGAAAAGCATTTCAGAGTCCTA	1281	
Db	1	GAAAGTTACATGGAAACTGGGTCAAACTGCACCTGGAGGAAACCATTCAGACATTCTG	60	
QY	1282	TTCAACCTGGGCTCCAAGTTTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTG	1341	
Db	61	CTTGGCCTGGGGACCAAAAGTACTCAGGCATTACCTGGGTGCCCTGAAGACCTGAGTCTG	120	
QY	1342	TCCCTGAGTGCAAAAGTGGCCCA-----	1364	
Db	121	TCCCTGAGCACACAAAGTGGCTCAATATGACATGTACTCCATGGCAGTGGGAACACTCATA	180	
QY	1365	-----GTTCTCACCCCTGCTCCTCTCAGCGTCCCACAGGCATGTCACAGAAAGGCT	1415	
Db	181	GTTTGGAGGTTCTCGCCCTGTTCTCTCTAGCACTCCACATGTGCTGTGCAGAAAGGCT	240	
QY	1416	GAGCTGGAAGTCCCACACTGTCACTCTCTGGGTTTTCTCTGCTCTTTATTGGTGATCCTG	1475	
Db	241	GAGCTGGATGTTCTCTGTGTGCGCTGTGTTTCGCTGCTCTTTTACTTGGTGTTTTG	300	
QY	1476	GTTCTTTCGGCCGTTTCACGTCATGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGT	1535	
Db	301	GTTCTTTCGGCCATTTCATGTCCTGCTGTCACCTCATCTGAGAGCTCGTGCTACCTCTGT	360	
QY	1536	GGCCTCTCGTGGCTGGCGGAGG	1558	
Db	361	AGCTCTCTGTTGGCTGGCAGTGGG	383	

RESULT 30	BC051059	3150 bp	mRNA	linear	HTC 22-APR-2003
LOCUS	Mus musculus mRNA similar to hypothetical protein FLJ20265 (cdna				
DEFINITION	clone IMAGE:5010465).				
ACCESSION	BC051059				
VERSION	BC051059.1	GI:30047881			
KEYWORDS	HTC.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 3150)				
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Shevchenko,Y., Sanchez,A., Whiting,M., Madan,A., Rodriguez,S., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
TITLE	JOURNAL				
	MEDLINE				
	PUBMED				
REFERENCE	2 (bases 1 to 3150)				
AUTHORS	Strausberg,R.				

ACCESSION BG389289
VERSION BG389289.1 GI:13282735
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 789)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10423 row: i column: 10
High quality sequence stop: 647.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4522449"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
Query Match 8.0%; Score 192.4; DB 1; Length 789;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1365 GTTCTCACCCCTGCTCCTGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGCTGGAA 1424
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
20 GTTCTCACCCCTGCTCCTGCTCAGCGTCCACAGGCACTGCAGAAAGGCTGAGCTGGAA 79
QY 1425 GTCCCACTGTCACTCTCTGGGTTTCTCTGCTCTTTTATTTGGTGATCCTGGTCTTTTCG 1484
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
80 GTCCCACTGTCACTCTCTGGGTTTCTCTGCTCTTTTATTTGGTGATCCTGGTCTTTTCG 139
QY 1485 GCCGTTACGTCATGTGTGCACCTCAGCTGAAAGTTCTGCTACTTCTGTGGCCTCTCG 1544
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
140 GCCGTTACGTCATGTGTGCACCTCAGCTGAAAGTTCTGCTACTTCTGTGGCCTCTCG 199
QY 1545 TGGCTGGCGGCGAG 1558
Db |||||||||||||||
200 TGGCTGGCGGCGAGG 213
RESULT 33
CG592530
LOCUS
DEFINITION CG592530 501 bp DNA linear GSS 02-OCT-2003
OST248759 Mus musculus 129Sv/Ev Mus musculus genomic clone
OST248759, Genomic survey sequence.
ACCESSION CG592530
VERSION CG592530.1 GI:37401614
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 501)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,

Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Slightenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
CONTACT: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1..501
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST248759"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
Query Match 8.0%; Score 191.7; DB 1; Length 501;
Best Local Similarity 57.3%; Pred. No. 0;
Matches 398; Conservative 0; Mismatches 79; Indels 217; Gaps 6;
QY 232 GGAGCCAGTTCTAACTGGACACCGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATGTT 291
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3 GGAGTCCGTTGAACTGGACCAAGCTGCC-CCACCTCTCTTCAGTAAAGTGGTTATGTG 61
QY 292 CTGATAGATGCCCTTGAGAGATGATTTTGTGTTGGTCAAAAGGTTGTAATTTATGCCC 351
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
62 TTGATAGATGCATTAGAGATGATTTTGTGTTGGTTCGAAAGGTGTGAAGTATATGCCC 121
QY 352 TACACAACTTACCTTGTGGAAGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCA 411
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
122 TACACAAAGTATCTGTAGAAAGGAGCATCTCATAGCTTTGTGGCTGAGGCAAGCCA 181
QY 412 CCTACAGTTACTATGCCTCGAATCAAGGCATGATGACGGGAGCCTTCCTGGCTTTGTC 471
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
182 CCCACAGTTACTATGCCTCGAATCA----- 206
QY 472 GACGTCATCAGGAACCTCAATTCTCCTGCTGCTGGAAGACAGTGTGATAAGACAAGCA 531
Db ----- 206
207 ----- 206
QY 532 AAAGCAGCTGGAAAAAGAAATAGTCTTTTATGGAGATGAAACCTGGGTTAAATATTCCCA 591
Db ----- 206
592 AAGCATTTTGTGGAATATGATGGAAACAACCTCATTTTTCGTGTCAGATTACACAGAGTG 651
Db -----AGGTG 211
652 GATAATAATGTCACGAGGCATTTGGATAAAGTATTAAAAAGAGGAGATTTGGACATATTA 711
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
212 GATAAAAATGTCACAAGGCATTTGGACAAGTATTAAAAAGAGGAGACTGGGATGTGTTA 271
QY 712 ATCTCCACTACCTGGGGCTGGACCACATTTGGCCACATTTTCAGGCCCCAACAGCCCCCTG 771
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
272 ATCTTCACTATCTAGGACTGGATCATTGGCCACATTTCTGGGCCCAACAGCCCCCTG 331
QY 772 ATTGGGCAGAAGCT-GAGCGAGATGGACAGCGTGTGATGAGATCCACACCTCACTGCA 830
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
332 ATTGGTCACAAGCTCTNCGNAAATGGACAGTNGCTGATGATAAATCCNCCCTTCACCTGCT 391
QY 831 GT--CGAAGGAGAGAGAGACGCTTTTACCCAAATTTGCTGGTCT-TTGTGGTGACCATGG 887
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
392 GNTCGAAAGGAGCTGAAAGACTCTCTTACCCAGTNCGCTGCTGCTCNGTNCGACCATGG 451

QY	1030	CTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTAGGAGCCTCCTATTCCCA	1089
Db	264	CTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTAGGAGCCTCCTATTCCCA	205
QY	1090	GTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAG	1149
Db	204	GTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAG	145
QY	1150	CTTAGTAAACTGTGCAAGAGAAATGTCCGTCATATGAAAAAGATCCTGG	1199
Db	144	CTTAGTAAACTGTGCAAGAGAAATGTCCGTCATATGAAAAAGAACTTTG	95
RESULT 38			
LOCUS	BX077539	764 bp	linear
DEFINITION	BX077539 AGENAE Rainbow trout normalized multi-tissues library (tcad) Oncorhynchus mykiss cdna clone tcad0004a.m.24 5prim, mRNA sequence.		
ACCESSION	BX077539		
VERSION	BX077539.1		
KEYWORDS	EST.		
SOURCE	Oncorhynchus mykiss (rainbow trout)		
ORGANISM	Oncorhynchus mykiss		
REFERENCE	Govoroun, M., Guiguen, Y. and Le Gac, F.		
AUTHORS	Construction and primary characterization of normalized cdna libraries in rainbow trout, Oncorhynchus mykiss		
TITLE	Unpublished (2003)		
JOURNAL	Contact: Guiguen Y		
COMMENT	INRA - SCRIBE		
FEATURES	Campus de beaulieu, RENNES cedex, 35042, France		
source	Tel: 02.23.48.50.09		
	Fax: 02.23.48.50.20		
	Email: Yann.Guiguen@beaulieu.rennes.inra.fr		
	Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this sequence.		
	Plate: 0004 row: m column: 24		
	Seq primer: T7.		
	Location/Qualifiers		
	1. .764		
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	liver, muscle, ovary, pituitary, testis"		
	/dev_stage="unknown"		
	/lab_host="DH10B"		
	/clone_lib="AGENAE Rainbow trout normalized multi-tissues library (tcad)"		
	/note="Vector: pT7T3D-pac; Clone distribution : AGENAE Resource centre. Francois PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, France"		
Query Match	6.8%;	Score 163.4;	DB 1;
Best Local Similarity	60.4%;	Pred. No. 0;	Length 764;
Matches 269;	Conservative	0;	Mismatches 176; Indels 0; Gaps 0;
QY	70	GTGTCCACATGCGGCTCGGGCTCCGGACTTTTCGCTACCTGTTGCGTAGCGATCGAGGTG	129
Db	251	GTCAGCAAAATGAGGATACGTTGCTGTTTTTGGCTGTTTTCGCTGTTTTCATCTACTGGAGGTA	310
QY	130	CTAGGGATCGCGTCTTCTTCGGGATCTTCCCGGCTCCCGTTCGTTCTCTCTGCCAGA	189
Db	311	TTAGGCATTGCTTGTCTTTCTTAGGGGATTTTCCCAGTCCCCTATCAAAATCTTCTTTTCA	370
QY	190	GCGGAACACGAGCGGAGCCCCACGCGCCCGAACCCTCGGCTGGAGCCAGTTCTAACTGG	249
Db	371	TCGAAGAGCAAGTTGTTCAGATGTTCCGCTGAACCCCTTTACCGGAAGATCCCTCAACTCC	430
QY	250	ACCACGCTGCCACCACCTCTCTTTCAGTAAAGTTGTTATTGTTCTGTAGATGCCTTGAGA	309
Db	431	TCCAAAGTCCCGACGCCCTTTTCAAGAGAGTAGTGATAGTTGATCGATGCTCTCAGG	490
QY	310	GATGATTTTGTGTTGGTCAAAGGGTGTGAAATTTATGCCCTACACAACTTACCTTGTG	369
Db	491	GAGGACTTTTGTGTTGGTCCAAATGGGAGAAAATACATGCCTTACATCAGGCACCTTGGTG	550
QY	370	GAAAAAGGAGCATCTCACAGTTTGTGGCTGAAAGCAAAAGCCACCTACAGTTACTATGCCT	429
Db	551	GAGAGGGGCTCCACATACAGCTTTGTGGCCCAAGGCAAGACCTCCTACAGTTACAATGCCC	610
QY	430	CGAATCAAGGCATTGATGACGGGGAGCCTTCCCTGCTTGTGCGACGTCATCAGGAACCTC	489
Db	611	AGAATCAAGGCCCTGACCACAGGTAGTATCCCGGCTTCATCGACGTTGGTGATGAACCTG	670
QY	490	AATTCTCCTGCACCTGCTGGAAGACA	514
Db	671	AACTCCCAGCGCTGCTGGAGGACA	695
RESULT 39			
LOCUS	AA356939	252 bp	mRNA
DEFINITION	EST65571 Jurkat T-cells III Homo sapiens cdna 5' end, mRNA sequence.		
ACCESSION	AA356939		
VERSION	AA356939.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.		
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cdna sequence		
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)		
MEDLINE	96026280		
PUBMED	7566098		
COMMENT	Contact: Kerlavage, AR		
	Bioinformatics		
	The Institute for Genomic Research		
	9712 Medical Center Drive, Rockville, MD 20850 USA		
	Tel: 3018699056		
	Fax: 3018699423		
	Email: arkerlav@tigr.org		
	For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)		
	Seq primer: M13 Reverse.		

FEATURES
source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):161322"
/db_xref="taxon:9606"
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/clone_lib="Jurkat T-cells III"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

Query Match
Best Local Similarity 6.7%; Score 160.4; DB 1; Length 252;
Matches 161; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1365 GTTCTCACCCCTGCTCCTGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGCTGGAA 1424
Db |||||
79 GTTCTCACCCCTGCTCCTGCTCAGCGTCCACAGGCACTGCAGAAAGGCTGAGCTGGAA 138
QY 1425 GTCCCACTGTCATCTCCTGGGTTTCTCTGCTCTTTTATTGTTGATCCTGGTCTTTTCG 1484
Db |||||
139 GTCCCACTGTATCTCCTGGGTTTCTCTGCTCTTTTATTGTTGATCCTGGTCTTTTCG 1484
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Db |||||
199 GCCGTTACGTCATTGTGTCACCTNAGCTGAAAGTTCGTGCTACTT 245

RESULT 40
BX077538/c

LOCUS
BX077538 744 bp mRNA linear EST 25-APR-2003
DEFINITION
(tcad) Oncorhynchus mykiss cdna clone tcad0004a.m.24 3prim, mRNA
sequence.
BX077538
BX077538.1 GI:27740957
EST.

ACCESSION
VERSION
KEYWORDS
SOURCE

Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 744)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cdna
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
Contact: Guiguen Y

REFERENCE
AUTHORS
TITLE

JOURNAL
COMMENT

INRA - SCRIBE
Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0004 row: m column: 24
Seq primer: T3.

FEATURES
source

Location/Qualifiers
1. .744
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
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differentiating gonads, interrenal, intestine, kidney,
liver, muscle, ovary, pituitary, testis"
/dev_stage="unknown"
/lab_host="DH10B"
/clone_lib="AGENAE Rainbow trout normalized multi-tissues
library (tcad)"
/note="Vector: pT7T3D-pac; Clone distribution : AGENAE
Resource centre. Francois PIUMI,

Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France"

Query Match
Best Local Similarity 6.6%; Score 158.2; DB 1; Length 744;
Matches 301; Conservative 0; Mismatches 183; Indels 46; Gaps 1;
QY 1064 ACAGTGTAGGGAGCCTCCTATTCCCACTGTGGAAGGAAGACCAATGAGAGAGCAGTTGA 1123
Db |||||
740 ACAGCGTGGGCCGACTCATCCAGCCCGTGGTTGACGAGGCCCTCGTCAGGGACCAAGCTGC 681
QY 1124 GATTTTACATTGTAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTCCCGTCAT 1183
Db |||||
680 GCTTCTGCACCTCAACGGCCACCACTGAGCTACCTGCTGAAGGACAGCATGCCAGCCT 621
QY 1184 ATGAAAAAGATCCTGGGTTGAGCAGTTTAAAAATGTCAGAAAGATTGCATGGGAACCTGA 1243
Db |||||
620 ATGAGAAAGAGGAGGGCTATGAGCAGTTCCTGTGGCAGAGAAGTCCCATGGTAAGTGGG 561
QY 1244 TCAGACTGTACTTGGAGGAAAAGCATTCAAGATCCTATTCAACCTGGGCTCCCAAGGTTT 1303
Db |||||
560 TGAAGCTAGTGGTGGAGGCAACACATCAGAGGTGCTGACCAACATGGGGAAGAGGTGT 501
QY 1304 TCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCAAGTGG--- 1360
Db |||||
500 TCAAGCAGTACCTGGAGGCCCTCAGGGCCCATGAGTGAAGCCCTCAGCAAGCAGCTGGGCA 441
QY 1361 -----CCAGTCTCACCCCTGC 1377
Db AATATGACATATATTCATGGTGGTGGCATGGTCTTGTCTTCCAGCTCCTTCTCCTCC 381
QY 1378 TCCTGCTCAGCGTCCCACAGGCACCTGCACAGAAAGGCTGAGTGGAAAGTCCCACTGTCTAT 1437
Db |||||
380 TGCTGTGCCCATGCCGAGGCACTGAGCAGTGCCTCAGAGGTGGATCTCCTGTGTCTCT 321
QY 1438 CTCCTGGGTTTCTCTGCTCTTTTATTTGGTGATCCTGGTCTTTCGGCCGTTTCACGTCA 1497
Db |||||
320 CTGCTCTGCTCTCGTGCCCTTCTACCTGCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTGG 261
QY 1498 TTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCTGTTG 1547
Db |||||
260 TGGTGTGCACCTCGGCCGAGAGCTCCTGTTACTTCTGCAGCCTCTCCTGG 211

RESULT 41
BUI30677

LOCUS
DEFINITION

BUI30677 739 bp mRNA linear EST 25-NOV-2002
603116501F1 CSEQCHL21 Gallus gallus cdna clone ChEST71b2 5', mRNA
sequence.
BUI30677
BUI30677.1 GI:25342596
EST.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Gallus gallus (chicken)
Gallus gallus

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 739)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)

PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLML1058 row: g column: 10
High quality sequence start: 15
High quality sequence stop: 584.

Location/Qualifiers
1. .758
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5010465"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

Query Match
Best Local Similarity 5.1%; Score 123; DB 1; Length 758;
Matches 241; Conservative 0; Mismatches 70; Indels 52; Gaps 5;

QY 1256 TGGAGGAAAAGCATT-CAGAAAGTCCTATTCAACCTGGCTCCAGGTTCTCAGGCAGTAC 1314
Db 50 TGGAGGAAAATCATTCGACAGACATTCTGCTGGCCTGGGACCAAGTACTCAGGCATTAC 109

QY 1315 C-TGGATGCTCTGAAGACGCTGAGCTTCTCCCTGAGTGCACAAAGTGGCCCA----- 1364
Db 110 CGTGGTGCCCTGAAGACCCCTGAGTCTCTCCCTGAGCACAAAGTGGTCAATATGACAT 169

QY 1365 -----GTTCTCACCCCTGCTCCTGCTCAG 1387
Db 170 GTACTCCATGGCAGTGGGAACACTCATAGTTTGGAGGTTCTCGCCCTGTTCTCCTTAG 229

QY 1388 CGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGAGTGGAAAGTCCCAGTGTATCTCTCTGG--G 1445
Db 230 CACTCCACATGTGCTGTGCAGAAAGGCTGAGCTGGATGTTCTCTGATAGTCGCTGATG 289

QY 1446 TTTTCTCTGCTCTTTTATTGGTGATCCTGTTCTTTCGGCCGTTTCACGTCATTTGTGTG- 1504
Db 290 TTTTGGCTGCTCTTTTACTTGGTGTATTAGTACATTTTCGCCCATTCATGTCCTGGTGTGC 349

QY 1505 -CACCTCAGCTGAAAGTTCTGCTGCTACTTCTGTGGCCCTCTGTTGGTGGCGGAGGCTGCC 1563
Db 350 ACACATCATCTGAGAGCTCTGCTGCTACCTCTGTAGCCCTCTGTTGGCTGGCAGTGGAGGCA 409

QY 1564 TTT 1566
Db 410 TGT 412

RESULT 43
BF442617 460 bp mRNA linear EST 01-DEC-2000
LOCUS 259515 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
DEFINITION BF442617
ACCESSION BF442617
VERSION BF442617.1 GI:11502709
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 460)
AUTHORS Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R.,

FEATURES
source
Location/Qualifiers
1. .739
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChEST71b2"
/dev_stage="36"
/lab_host="DH10B"
/clone_lib="CSEQCHL21"
/note="Organ: trunks; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites [5'ggccgcgtgagcccgatccggaataaaag] [5'aattcttttttcggtatccggggtgcagc]"

Query Match
Best Local Similarity 6.4%; Score 153.8; DB 1; Length 739;
Matches 245; Conservative 0; Mismatches 117; Indels 2; Gaps 2;

QY 788 GCGAGATGACAGCGTGTG-ATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAG 846
Db 12 GTGAATGACAAACGCTTGTGAACGAAGATTCATTTCTCTGCTGTCAGAGGAGGAGAG 71

QY 847 ACGCCTTTACCAATTTGCTGTTCTTTGTGGTGACCATGG-CATGCTGAAACAGGAAG 905
Db 72 GCTTCTCTGCTAGTTTGTGTTTGTGGGATCATGGAGATGTTCTGAAACAGGCAG 131

QY 906 TCACGGGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTATCAGTTCTGCGTT 965
Db 132 TCATGGTGTCTTTCAGAAAGATGAAGTGACACACCGCTGCTGTTTATCAGCTCTGCTTT 191

QY 966 TGAAGGAAACCCGGTGATATCCGATATCCAGACGTCCTCAATAGACGGATGTGGCTGC 1025
Db 192 TGAAGAGAAAGTGGTCTTAACCCCACTTGAACCTGTGCAACATCTGATGGCCTAG 251

QY 1026 GACACTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCCTATT 1085
Db 252 TACACGGGCAGTAGTCTTGGTCTACCAATTTCAAGAAACAATGTTGGGAACATTATATT 311

QY 1086 CCCAGTTGTGGAAGAACCAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGT 1145
Db 312 ACCAGTTGTGGGAAGCAAAACAATGAGAGAACAACTATGAACAAATTTTGATAGTATT 371

QY 1146 GCAG 1149
Db 372 GGAG 375

RESULT 42
BI080925 758 bp mRNA linear EST 20-JUN-2001
LOCUS 602878836F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5010465 5', mRNA sequence.
DEFINITION BI080925
ACCESSION BI080925
VERSION BI080925.1 GI:14499255
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 758)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

TITLE Quackenbush,J. and Keele,J.W.
JOURNAL Porcine gene discovery by normalized cdna-library sequencing and
MEDLINE EST cluster assembly
PUBMED Mamm. Genome 13 (8), 475-478 (2002)
COMMENT 22213789
12226715
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 90 row: G column: 23
Seq primer: APTTAGGTGACACTATAG.
Location/Qualifiers
1. .460
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2P1G"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

FEATURES
source

Query Match 4.9%; Score 116.4; DB 1; Length 460;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 135; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 68 GCGTGTCACGATCGGCTGGCTCCGGACTTTCGCTACCTGTTGCGTAGCGATCGAGG 127
Db 54 GGGTGGGCACATCGGCTGGCTCGGGACCTTCGCCGCTGCTGCGTAAGATCGAGG 113
QY 128 TGCTAGGATCGGCTCTTCCTTCGGGGATTCTTCCCGCTCCGTTTCGTTCCCTCTGCCA 187
Db 114 TGCTCGGCTCGGCTCTTCCTTCGGGGATTCTTCCCGCTCCTGTTCTTCCTCTCTG 173
QY 188 GAGCGGAACACGAGCGGAGCCCGAGCCCGGACCCGACCCCTCGGCTGG 233
Db 174 GCACGGAGCGCAAGTAGAGCACCCAGCCCGCCGACCTCGACTGG 219

RESULT 44

AL913388
LOCUS AL913388 PUR-Z1+Z2 510 bp mRNA linear EST 18-SEP-2002
DEFINITION AL913388 Danio rerio cdna clone 068-E03-2, mRNA sequence.
ACCESSION AL913388
VERSION AL913388.1 GI:23178658
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 510)
AUTHORS Lo,J., Lee,S., Xu,M., Liu,F., Ruan,H., Eun,A., He,Y., Ma,W.,
Wang,W., Wen,Z. and Peng,J.
15000 unique zebrafish EST clusters and their future use in
microarray for profiling gene expression patterns during
embryogenesis
Genome Res. 13 (3), 455-456 (2003)
JOURNAL 22505427
MEDLINE 12618376
PUBMED
COMMENT Contact: Peng J
Lab of Functional Genomics
Institute of Molecular and Cell Biology

FEATURES
source

30 Medical Drive, Singapore, 117609, Singapore
Email: pengjr@imcb.a-star.edu.sg
Clone requests: pengjr@imcb.a-star.edu.sg.
Location/Qualifiers
1. .510
/organism="Danio rerio"
/mol_type="mRNA"
/strain="local_wildtype"
/db_xref="taxon:7955"
/clone="068-E03-2"
/tissue_type="whole embryo or fish"
/dev_stage="mixed stages"
/clone_lib="PJR-Z1+Z2"

Query Match 4.8%; Score 114.6; DB 1; Length 510;
Best Local Similarity 57.5%; Pred. No. 0;
Matches 241; Conservative 0; Mismatches 174; Indels 4; Gaps 2;
QY 61 CAGCCTAGCGTGTCACGATCGCGCTGGGCTCCGGGACTTTCGTACCTGTGCGTAGCG 120
Db 92 CAGCTACTGATCTTAATCATGAGCTGAGCTCTTCAGTATTGCTTTATTGTCTCATA 151
QY 121 ATCGAGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCGGGCTCCGTTCTGTTCC 180
Db 152 CTTGAGATTGTGTCATCGCTCTTTCCTGAGAGGATCTTCCCTGTTCCCTGTCAAATCC 211
QY 181 TCTGCCAGAGCGGAACACGAGCGGAGCGGAGCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGT 240
Db 212 TCCTTTTCAGCCAAAGAGCAAGTACTGATATTTCCTCAGAGCCACAGACAGGTAATAAT 271
QY 241 TC--TAACCTGGACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATA 297
Db 272 GCAGTTAACTCCAGCCGAGCGCGCGGCTGCTGTTCAAGCGTGTGGTATAGTCTCTGATC 331
QY 298 GATGCCTTGAGAGATGATTTTGTTGGTCAAGGGTGTGAAATTTATGCCCTACACA 357
Db 332 GACGCTCTCAGGGAAGA-CTTGTTGTTGAGTCTCTGATGACGGAGGTTTATGCCCTACACC 390
QY 358 ACTTACCTTGGAAGAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACCTACA 417
Db 391 AGACACGTGGTGGAGAAAGGCTCGTCTCACAGCTTCATCGCCAAAGCCAGACCGCCACC 450
QY 418 GTTACTATGCCTCGAATCAAGGCATGTGATGACGGGGAGCCTTCTCGCTTGTCTGACGT 476
Db 451 GTCACCATGCCAGAATTAAAGGCTTTGACCACCGGCAGCATCCCTGGATTCATAGACGT 509

RESULT 45
CE024824

LOCUS CE024824 720 bp DNA linear GSS 24-SEP-2003
DEFINITION tigr-gss-dog-17000322355404 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE024824
VERSION CE024824.1 GI:35040988
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 720)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
JOURNAL 22875432
MEDLINE 14512627
PUBMED
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208

align44

Tue Sep 7 08:53:52 2004

1438 CTCCTGGGTTTCTC--TGCTCTTTTATTGGTGATCCTGGTTCTTCGGCCGTTACAGT 1495
1 CTCCTGGGTTTCTCGTGGCTCTTTTATTGGTGATCCTGGTTCTTCGGCCGTTACAGT 60

1496 CATTGTGTGCACCTCAGCTGAAAGTTCTGTCTTCTGTGGCTCTCTGTGGCTGGCGGC 1555
61 CATTGTGTGCACCTCAGCTGAAAGTTCTGTCTTCTGTGGCTCTCTGTGGCTGGCGGC 120

1556 AGG 1558
121 AGG 123

RESULT 47
BQ360060
LOCUS 122 bp mRNA linear EST 20-MAY-2002
DEFINITION MR3-HN0166-310101-002-f02 HN0166 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ360060
VERSION BQ360060.1 GI:21028397
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 122)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-HN0166-310101-002-f02&t3=2001-01-31&t4=1)
Seq primer: puc 18 forward.

FEATURES
Location/Qualifiers
1..122
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HN0166"
/note="Organ: head normal; Vector: puc18; Site: 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Query Match 4.5%; Score 107.4; DB 1; Length 122;
Best Local Similarity 94.9%; Pred. No. 0;
Matches 111; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2271 CTGTGCCAGCTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTGCTATTGAAT 2330
DB 5 CTCTGTGCAGCTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTGCTATTGAAT 64

Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1..720
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"

Query Match 4.6%; Score 110.4; DB 1; Length 720;
Best Local Similarity 82.9%; Pred. No. 0;
Matches 126; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

832 TCGAAGGAGAGAGAGACGCCCTTTACCAATTGCTGGTCTTTGTTGGTGACCATGGCATG 891
19 TTGTAGGAGAGAGAAACTCTTGATCCCAATTGCTGGTCTCTGTGTGATCACGGCATG 78

892 TCTGAAACAGGAAGTCACGGGGCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTA 951
79 TCTGAAACTGGCGGTTCATGGGGCTCTTCCATGGAGGAGCTTAACACCGCCTGATCTTA 138

952 ATCAGTTCTGCGTTTGAAGGAAACCCGGTGA 983
139 ATCAGTTCTGCAATTGAAAGAAACCTGGTGA 170

RESULT 46
BE897861
LOCUS 934 bp mRNA linear EST 20-OCT-2000
DEFINITION BE897861 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925494 5', mRNA sequence.

ACCESSION BE897861
VERSION BE897861.1 GI:10363749
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 934)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9764 row: p column: 07
High quality sequence stop: 704.

FEATURES
Location/Qualifiers
1..934
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3925494"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life Technologies."

Query Match 4.5%; Score 108.4; DB 1; Length 934;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 120; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Db 779 AGGACTTGTGAGCGTCTGGAGATGACACAC-----TGCTGGTAGTGGCTG 826
QY 878 GTGACCATGGCATGCTCTGAAACAGGAAGTCACGGGCGCTCTCCACCGAGGAGGTGAATA 937
Db 827 GGGACCATGGGATGACCAACAATGGAGACCATGGAGGGACAGTAGCTGGAGGTCTCAG 886
QY 938 CACCTCTGATTTT 950
Db 887 CTGCTCTCTTTCT 899

RESULT 53
BZ270849
LOCUS CH230-509L24.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
DEFINITION CH230-509L24, genomic survey sequence.
ACCESSION BZ270849
VERSION BZ270849
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 466)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
TITLE Rat BAC End Sequences from Library CHORI-230 MboI segment
JOURNAL Unpublished (1999)
COMMENT Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/oreringinformation.htm>). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 509 row: L column: 24
Seq primer: Sp6
Class: BAC ends.
FEATURES Location/Qualifiers
source 1..466
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-509L24"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"

Query Match 4.3%; Score 102.5; DB 1; Length 466;
Best Local Similarity 73.7%; Pred. No. 0;
Matches 143; Conservative 0; Mismatches 50; Indels 1; Gaps 1;

QY 1197 TGGGTTTGAGCAGTTTAAATGTCAGAAAGATTGCGTGGGAACTGGATCAGACTGTACTT 1256
Db 1 TGGATTTTGAGCAGTTTAAATATGAGAAAGGTTGCGTGGGAACTGGTCAAACTGCACCT 60
QY 1257 -GGAGGAAAGCATTTCAGAGTCTTATTCAACCTGGGCTCCAAGGTTCTCAGGCAGTACC 1315
Db 61 GGAAGAAACCATTCAGACATCTGCTTGGCTTGGGACCAAAAGTACTCAGGCAGTACC 120

QY 1316 TGGATGCTCTGRAGACGCTGAGCTTGTCCTCTGAGTGCACAAGTGGCCCACTTCTCACCCCT 1375
Db 121 TGGGTGCCCTGRAGACCCCTGAGTCAGTCCCTGAGCACACAAGTGGCTCACTATGACATCT 180
QY 1376 GCTCCTGCTCAGCG 1389
Db 181 ACTCAATGGCAGTG 194

RESULT 54
BJ434815/c
LOCUS BJ434815 Dictyostelium discoideum cDNA library, VF Dictyostelium
DEFINITION BJ434815 Dictyostelium discoideum cDNA clone ddv25e05 3', mRNA sequence.
ACCESSION BJ434815
VERSION BJ434815
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum

REFERENCE 1 (bases 1 to 560)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the vegetative
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES Location/Qualifiers
source 1..560
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddv25e05"
/sex="mat A"
/dev_stage="Growth phase"
/clone_lib="Dictyostelium discoideum cDNA library, VF"

Query Match 4.2%; Score 99.4001; DB 1; Length 560;
Best Local Similarity 55.4%; Pred. No. 0;
Matches 190; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 479 TCAGGAACCTCAATCTCTCTGCACTGCTGGAGAGACAGTGTGATAAGACACAAAGCAG 538
Db 557 TTAATAATTTCAATAGTCNACCATAAGGAGGATAACATCTATATCAAAATGAACAAT 498
QY 539 CTGGAAAAACAATAGTCTTTTATGGAGATGAAACCTGGTTAAATTTCCCAAAGCATT 598
Db 497 CAAATAATCAATGTTATTCTTTGGCGATGATACCTGGTTAAACTATTCCCTGACTACT 438
QY 599 TTGTGGAATATGATGGAACAACCTCATTTTTCGTGTCAGATTACACAGAGGTGGATAATA 658
Db 437 TCAACGACATGATGGTACAACTAGTTTNTATGTTGCCGATACGTAGAGAGTTGATTAA 378
QY 659 ATGTCACGAGGCATTGGAATAAAGTATTAAAGAGGAGATTTGGACATATTATCTCTCC 718
Db 377 ATGTCACATAGACATTTAGAACCAAGATTAAATAATGATTTGGGATGTTATGTTTTTAC 318
QY 719 ACTACCTGGGCTGGACCACATTTGCCACATTTTCAGGGCCCAACAGCCCCCTGATTGGGC 778
Db 317 ATTACCTTGGTTAGATCATATAGGTCAATTTGGAGGCTCCACATTTCTTAATCTAATGAAC 258
QY 779 AGAAGCTGACGAGATGGACAGCGTGTGATGAAGATCCACAC 821
Db 257 CAAACAAAAAGAAATTGATAATATCATTAATAATTATACATAC 215

RESULT 55

Tue Sep 7 08:53:52 2004

RESULT 57
AW862654
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 545)
Zhang, J., Underwood, L.E. and D'Ercole, A.J.
Identification of fasting inducible genes from rat liver by
suppression subtractive hybridization
Unpublished (2000)
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USA
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Fax: 919 966 2423
Email: jihui_zhang@med.unc.edu.
Location/Qualifiers
1. .545
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
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/sex="male"
/dev_stage="five-week-old postnatal, fasting for 48 hours"
/clone_lib="Rat Liver Subtracted cDNA Library"
/note="Organ: liver; Vector: pGEM-T; This subtracted cDNA
library was constructed by inserting desired
differentially expressed sequences into a plasmid pGEM-T,
followed by transforming E. coli strain JM109.
Differentially expressed sequences from fasted rat liver
were generated by suppression subtractive hybridization,
in which mRNA from fasted rats was used as a test and
mRNA from control fed rats as a reference. A standard
tailing procedure with Taq DNA polymerase was employed to
introduce 3'-A overhang to the desired cDNAs before
cloning into pGEM-T. Subtraction efficiency of this
library was shown to be >60%. The average insert size of
clones in this library is 369 bp (20 bp)."

FEATURES
source

Query Match 3.9%; Score 93.8002; DB 1; Length 545;
Best Local Similarity 51.8%; Pred. No. 0;
Matches 212; Conservative 0; Mismatches 197; Indels 0; Gaps 0;
QY 398 CTGAAGCAAGCCACCTACAGTTACTATGCTCGAATCAAGGCATTGATGACGGGAGCC 457
Db 9 CTCAGGTGGATCCCCCAACACCATGCAGCGTCTGAAGGCTCTCACCGCTGGCTCGC 68
QY 458 TTCCTGGCTTTGTCGACGTCATCAGGAACCTCAATTCTCTGCACTGCTGGAAGACAGTG 517
Db 69 TGGCGACTTTTATTGATGCCGGCAGTAACCTTCGCCAGCCATGCTATTGTGAAGATAATC 128
QY 518 TGATAAGACAAGCAAGCAGCTGGAAAAAGAAATAGTCTTTTATGGAGATGAAACCTGGG 577
Db 129 TCATCAAGCAGCTCACCAGTGCAGGAAGCGGTAGTCTTTCATGGGAGATGATACCTGGA 188
QY 578 TTAATATTCCCAAAGCATTTTGTGGATATGATGGAACAACCTCATTTTTCGTGTGTCAG 637
Db 189 AAGACCTTTTCCCTGGAGCATTTTCCCAAGCTTTCTTCTCTCATCTTCAATGTCTAGAG 248
QY 638 ATTACACAGAGTGGATAAATATGTCACGAGGCATTTGGATAAAGTATTAATAAAGAGGAG 697
Db 249 ACCTACACACAGTGGATAAATGTCATCTTACCTCTATCTTACCTACCTAGGACAGCGGCG 308

QY 698 ATTGGGACATATTATCTCCACTACCTGCTGGGCTGGACCACTTGGCCACATTCAGGGC 757
Db 309 CCTGGGATGTCTGATGCTCACTTCTCTGGTGTGGATCATTTGTTCAATAGCATGGCC 368
QY 758 CCAACAGCCCTGATTTGGCAGAGCTGAGCGAGATGACAGCGTGTCT 806
Db 369 CTCACCACCTGAAATGGCCAAAGAACTTAGCCAGATGGACCAGGTGAT 417
RESULT 58
AY408632
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus HCM3288 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY408632
AY408632.1 GI:39764603
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3282)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 3282)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Query Match 3.8%; Score 90.6002; DB 1; Length 3282;
Best Local Similarity 51.3%; Pred. No. 0;
Matches 210; Conservative 0; Mismatches 199; Indels 0; Gaps 0;
QY 398 CTGAAGCAAGCCACCTACAGTTACTATGCTCGAATCAAGGCATTGATGACGGGAGCC 457
Db 368 CTCAGGTGGACCCCCACGACCCACCATGCAGCGTCTAAAGGCTCTCACCACTGGCTCGC 427
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QY 578 TTAATATTCCCAAAGCATTTTGTGGAAATATGATGGAACAACCTCATTTTTCGTGTGTCAG 637
Db 548 GAGACCTTTCCCGGAGCGCTTTTCTCAAGCTTTCTTCTTCTCATCTTCAATGTCTAGAG 607
QY 638 ATTACACAGAGTGGATAAATATGTCACGAGGCATTTGGATAAAGTATTAATAAAGAGGAG 697
Db 608 ACCTGCACACAGTGGATAACGGCATCTTGGAAACACCTCTATCTTACCTGACGGCGTT 667

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